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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:31:42 ; Search time 61.6875 Seconds  
(without alignments)  
273.318 Million cell updates/sec

Title: US-09-913-927D-2

Perfect score: 262

Sequence: 1 MEQAPEDQGPQREPYNEWTL.....SEAVRHPPRIWLNLGQHIY 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	262	100.0	47	3 AAB10686	Aab10686 HIV-1 reg
2	262	100.0	60	7 ABR42471	AbR42471 HIV viral
3	262	100.0	79	2 AAR48961	Aar48961 NL4-3 VPR
4	262	100.0	96	2 AAR48963	Aar48963 HIV VPR.
5	262	100.0	96	2 AAW53040	Aaw53040 HIV-1 pol
6	262	100.0	96	3 AAB10049	Aab10049 HIV-1 vpr
7	262	100.0	96	3 AAB10685	Aab10685 HIV-1 reg
8	262	100.0	96	5 AAE16129	Aae16129 Human imm
9	262	100.0	96	5 ABP56175	Abp56175 HIV-1 vir
10	262	100.0	96	7 ADD01277	Add01277 HIV-1 vpr
11	262	100.0	96	8 ADF46812	Adf46812 HIV-1 vpr
12	262	100.0	96	8 ABM79669	Abm79669 HIV-1 Vpr
13	256	97.7	96	6 ABR55491	AbR55491 Amino aci
14	255	97.3	96	3 AAB69306	Aab69306 HIV-1 non
15	252	96.2	96	5 AAU80187	Aau80187 HIV-1 Vpr
16	251	95.8	78	2 AAW99828	Aaw99828 HIV HXB2
17	251	95.8	96	2 AAW99823	Aaw99823 HIV L68S
18	251	95.8	96	2 AAW99824	Aaw99824 HIV H71C
19	251	95.8	96	2 AAW99821	Aaw99821 HIV L64S
20	251	95.8	96	2 AAW99826	Aaw99826 HIV G75A
21	251	95.8	96	2 AAW99820	Aaw99820 HIV A59P
22	251	95.8	96	2 AAW99825	Aaw99825 HIV H71Y
23	251	95.8	96	2 AAW99827	Aaw99827 HIV C76S
24	251	95.8	96	2 AAW99815	Aaw99815 HIV Vpr w
25	251	95.8	96	2 AAW99822	Aaw99822 HIV L67S

#### ALIGNMENTS

##### RESULT 1

AAB10686  
ID AAB10686 standard; peptide; 47 AA.

XX AAB10686;

XX 19-JAN-2001 (first entry)

DE HIV-1 regulatory virus protein R peptide svpr1-47.

XX Regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity;  
KW structural analysis; cell cycle arrest.

XX Synthetic.

OS Human immunodeficiency virus 1.

XX Key Location/Qualifiers

PH Modified-site 47

FT /note= "C-terminal amide"

XX WO200049038-A2.

XX 24-AUG-2000.

XX 19-FEB-2000; 2000WO-DE000525.

XX 19-FEB-1999; 99DE-01008752.

XX 19-FEB-1999; 99DE-01008766.

XX (SCHU/) SCHUBERT U.

XX (HENK/) HENKLEIN P.

XX (WRAY/) WRAY V.

PI Schubert U, Henklein P, Wray V;

XX WPI; 2000-565367/52.

PT New synthetic peptides from the Vpr protein of human immune deficiency virus, useful e.g. for therapy and diagnosis, have good solubility in water.

XX Claim 3.2; Page 5; 35pp; German.

CC This invention describes novel synthetic peptides (I) derived from the regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-1) which have antiviral activity and can be used for gene therapy. (I) is used for therapeutic and/or diagnostic purposes, especially in biological assays, for development of serological tests or enzyme-linked

Aar94547 Fragment  
Aay53250 SIV Vpr p  
Aab85995 Amino aci  
Aao30521 HIV vpr m  
Aao30515 HIV vpr n  
Aao30516 HIV vpr m  
Aao30517 HIV vpr m  
Aao30518 HIV vpr m  
Aao30519 HIV vpr m  
Aao30520 HIV vpr m  
Adn34417 HIV prote  
Aar94544 Native Vp  
Aaw99818 HIV A30S  
Aay53247 HIV-1 LAI  
Aap20070 Human imm  
Aap91048 Transcrip  
Aap20078 Human imm  
Aap81856 Sequence  
Aar10174 Rap (R) p  
Aaw99819 HIV A30L

CC immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in  
 CC blood), to raise specific antibodies and antisera (especially those  
 CC reactive with specific epitopes), and as antiviral agents. (I) can also  
 CC be used in screening for potential Vpr antagonists (i.e. compounds that  
 CC modulate interaction of Vpr with cellular factors, transcription-  
 CC activating properties of Vpr, transport of Vpr and its incorporation into  
 CC viral particles, Vpr-induced cell cycle arrest, and cytotoxic and ion-  
 CC channel activities of Vpr). (I) is used to establish cell or animal  
 CC models for studying pathogenicity of Vpr, for structural analysis of Vpr  
 CC and its domains, for in vitro assembly of new vectors for gene therapy,  
 CC in vitro or in vivo, for complementing the function of Vpr-defect mutants  
 CC in cell cultures, and to reduce flexibility of Vpr induced by the N-  
 CC terminal domain. Synthetic (I), are soluble in water and can be  
 CC formulated as highly concentrated solutions (mmolar) without protein  
 CC aggregation, so are well suited to analysis by nuclear magnetic  
 CC resonance, X-ray or circular dichroism techniques. (I) adopt a folded  
 CC structure, have biological activity comparable to that of viral Vpr, and  
 CC can be produced, at high purity, on the milligram scale. This sequence  
 CC represents the synthetic HIV-1 derived Vpr peptide sVpr1-47 which is used  
 CC in the method of the invention

XX Sequence 47 AA;

Query Match 100.0%; Score 262; DB 3; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLELLELSEAVRHFPRIWHLNLGQHIY 47  
 |||||  
 Db 1 MEQAPEDQGPQREPYNEWTLLELLELSEAVRHFPRIWHLNLGQHIY 47

RESULT 2  
 ABR42471  
 ID ABR42471 standard; protein; 60 AA.

XX ABR42471;  
 AC ABR42471;  
 DT 11-AUG-2003 (first entry)  
 XX HIV viral protein R (aa-160).  
 DE HIV; viral protein R; Vpr; lentiviral R protein; anti-HIV; virucide.  
 KW Human immunodeficiency virus.  
 OS

XX Key Location/Qualifiers  
 FH 17..29  
 FT Region /note= "alpha-helix 1"  
 FT 36..47  
 FT Region /note= "alpha-helix-2"  
 FT

XX WO2003038056-A2.

PN 08-MAY-2003.

XX 31-OCT-2002; 2002WO-US035110.

XX 02-NOV-2001; 2001US-0350168P.

XX (REGC ) UNIV CALIFORNIA.

XX Sherman M, Greene WC, Schubert U, Wray V, Tessmer U, Henklein P;  
 PI Bruns K;

XX WPI; 2003-468412/44.

XX Identifying an agent that induces Vpr loss in a lentivirus-infected cell,  
 PT useful for treating lentiviral infections by determining the effect of  
 PT the test agent contacted with a cell that produces Vpr protein on the  
 PT level of Vpr in the cell.

XX Example 5; Fig 4; 44pp; English.

XX The present sequence is that of amino acids 1-60 of HIV viral protein R  
 CC (vpr, also called lentiviral R protein). Vpr is incorporated into the HIV  
 CC virion and helps to target the viral preintegration complex to the  
 CC nucleus in nondividing cells through its nuclear localisation signal. It  
 CC is also responsible for arresting HIV infected cells in the G2 phase of  
 CC the cell cycle, which results in increased virus production. The  
 CC invention provides methods for identifying compounds that induce loss of  
 CC Vpr in a eukaryotic cell, and methods for identifying compounds that  
 CC inhibit a peptide/prolyl cis/trans isomerase activity of a protein that  
 CC catalyses cis-trans isomerization of cis-peptidylprolyl bonds in Vpr.  
 CC Such compounds are useful for treating lentiviral infections, including  
 CC HIV infections

XX Sequence 60 AA;

Query Match 100.0%; Score 262; DB 7; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLELLELSEAVRHFPRIWHLNLGQHIY 47  
 |||||  
 Db 1 MEQAPEDQGPQREPYNEWTLLELLELSEAVRHFPRIWHLNLGQHIY 47

RESULT 3  
 AAR48961  
 ID AAR48961 standard; protein; 79 AA.

XX AAR48961;

DT 25-MAR-2003 (revised)

DT 12-SEP-1994 (first entry)

XX NL4-3 VPR N-terminal peptide.

XX HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;  
 KW naturally occurring virus; NOV; translation; replication; infectivity;  
 KW hepatitis B; HIV-2; SIV; flip-over PCR.

XX Synthetic.

XX WO9403596-A1.

PD 17-FEB-1994.

XX 30-JUL-1993; 93WO-US007179.

XX 30-JUL-1992; 92US-00921104.

XX (UYHA-) UNIV HAWAII.

XX Hu W, Wang J;

XX WPI; 1994-065685/08.

XX N-PSDB; AAQ57688.

XX New antisense viruses and anti-sense-ribozyme viruses - used for treating  
 PT or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.

XX Disclosure; Page 108; 167pp; English.

XX This sequence is encoded by a PCR fragment of NL4-3 and represents the N-  
 CC terminal peptide fragment of the full length VPR protein. The DNA  
 CC encoding this fragment was ligated into ClaI/SalI digested pX and the  
 CC corresponding plasmid was used to produce the antisense virus of the  
 CC invention. Antisense or truncated RNAs expressed by these viruses bind to  
 CC the mRNAs expressed by the naturally occurring viruses (NOVs) and prevent  
 CC the mRNAs from being translated into proteins, thereby preventing the NOV  
 CC from replicating. The antisense viruses maintain the infectivity of the  
 CC NOVs, allowing antisense RNAs to reach the mRNAs of the natural viruses.  
 CC Antisense viruses such as these may be used for treating or preventing a  
 CC viral infection, particularly HIV-1, HIV-2 or SIV infection or hepatitis

CC B infection. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 79 AA;  
 Query Match 100.0%; Score 262; DB 2; Length 79;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRIWLHNLGQHIY 47  
 |||||  
 Db 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRIWLHNLGQHIY 47

## RESULT 4

AAR48963  
 ID AAR48963 standard; protein; 96 AA.

XX AAR48963;

XX 25-MAR-2003 (revised)

DT 12-SEP-1994 (first entry)

XX HIV VPR.

DE HIV VPR.

XX HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;  
 KW naturally occurring virus; NOV; translation; replication; infectivity;  
 KW hepatitis B; HIV-2; HIV; flip-over PCR.

XX Synthetic.

XX MO9403596-A1.

PN 17-FEB-1994.

XX 30-JUL-1993; 93WO-US007179.

PR 30-JUL-1992; 92US-00921104.

XX (UYHA-) UNIV HAWAII.

XX Hu W, Wang J;

XX WPI; 1994-065685/08.

DR N-PSDB; AAQ48962.

XX New antisense viruses and anti-sense-ribozyme viruses - used for treating  
 PT or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.  
 XX Disclosure; Page 111; 167pp; English.

XX This sequence represents the "perfect" VPR protein encoded by the PCR  
 CC fragment of pX-CS which encodes the truncated gag gene and the "perfect"  
 CC vpr gene. The cDNA fragment encoding this protein was used to produce the  
 CC antisense virus of the invention. Antisense or truncated RNAs expressed  
 CC by these viruses bind to the mRNAs expressed by the naturally occurring  
 CC viruses (NOVs) and prevent the mRNAs from being translated into proteins,  
 CC thereby preventing the NOV from replicating. The antisense viruses  
 CC maintain the infectivity of the NOVs, allowing antisense RNAs to reach  
 CC the mRNAs of the natural viruses. Antisense viruses such as these may be  
 CC used for treating or preventing a viral infection, particularly HIV-1,  
 CC HIV-2 or SIV infection or hepatitis B infection. (Updated on 25-MAR-2003  
 CC to correct PN field.)

SQ Sequence 96 AA;  
 Query Match 100.0%; Score 262; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRIWLHNLGQHIY 47  
 |||||  
 Db 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRIWLHNLGQHIY 47

## RESULT 5

AAW53040  
 ID AAW53040 standard; peptide; 96 AA.

XX AAW53040;

XX 17-OCT-2003 (revised)

DT 17-JUL-1998 (first entry)

XX HIV-1 polypeptide.

DE HIV-1 polypeptide.

XX Recombinant plant virus; HIV-1; protein production; immunisation;  
 KW fusion capsid protein; alfalfa mosaic virus; ilarvirus; pathogen;  
 KW rhabdovirus.

XX Human immunodeficiency virus 1.

XX WO9808375-A1.

PN 05-MAR-1998.

XX 28-AUG-1997; 97WO-US015200.

PR 28-AUG-1996; 96US-00704856.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Koprowski H, Hooper DC, Yusibov V, Modelska A;

XX WPI; 1998-179070/16.

XX Production of poly:peptide(s), particularly for use in vaccines - by  
 PT expression as fusion proteins with plant virus capsid protein in plant  
 PT cells infected with virus.  
 XX Disclosure; Page 4; 63pp; English.

XX This sequence is a HIV-1 polypeptide that can be used in a recombinant  
 CC plant virus used in the process of the invention. The process is for  
 CC administering a polypeptide to an animal comprising: (a) infecting a  
 CC plant cell with recombinant plant virus nucleic acid that will be  
 CC processed in a plant cell to produce a fusion capsid protein (FCP), the  
 CC FCP comprises a plant virus capsid protein (PVCp) and a polypeptide that  
 CC is not a PVCp, the PVCp being an alfalfa mosaic virus (AlMV) capsid  
 CC protein (CP) or ilarvirus CP thereby creating a infected cell; (b)  
 CC cultivating the infected cell, or a derivative cell derived from the  
 CC infected cell, under conditions where the infected cell or derivative  
 CC cell makes the FCP; and (c) administering the FCP or a portion to an  
 CC animal. The recombinant plant virus can also be used for production of  
 CC polypeptides. The method is used particularly for the production of  
 CC polypeptides which can be used for immunisation against pathogens such as  
 CC rhabdovirus or HIV. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 96 AA;

Query Match 100.0%; Score 262; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRIWLHNLGQHIY 47  
 |||||  
 Db 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRIWLHNLGQHIY 47

## RESULT 6

AAAB10049  
 ID AAAB10049 standard; protein; 96 AA.

XX AAAB10049;

XX 12-SEP-2003 (revised)

DT 02-NOV-2000 (first entry)

XX HIV-1 vpr protein.  
 DE Glycoprotein; gag; pol; GP-1; GP-2; anti-HIV; cytostatic; gene therapy;  
 KW treatment; infectious disease; HIV; AIDS; neoplasm; carcinoma; melanoma;  
 KW vpr protein.  
 XX Human immunodeficiency virus 1.  
 OS  
 XX EF1006196-A2.  
 PN  
 XX 07-JUN-2000.  
 PD  
 XX 25-NOV-1999; 99EP-00250415.  
 PF  
 XX 26-NOV-1998; 98DE-01056463.  
 PR  
 XX (PETT-) PETTE INST HEINRICH.  
 PA  
 XX Von Laer MD;  
 PI  
 XX WPI; 2000-378268/33.  
 DR  
 XX N-PSDB; AAA40298, AAB10053, AAB10054.  
 DR  
 XX New retroviral packing cell useful as pharmaceutical carrier in gene  
 PT therapy for treatment of HIV and neoplasms, comprises retroviral genes  
 PT and glycoproteins.  
 PT  
 XX Disclosure; Page 44; 69pp; German.  
 PS  
 XX This invention describes a novel retroviral packing cell (I), comprising  
 XX the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV  
 CC coding gene gp, or a part of these. The products of the invention have  
 CC anti-HIV and cytostatic activity and can be used for gene therapy. (I) is  
 CC useful for in vitro infection of cells, especially hematopoietic stem  
 CC cells, for expression of transgenes in cells and as a pharmaceutical  
 CC carrier for gene therapy. (I) is therefore useful in the treatment of  
 CC infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and  
 CC other diseases. This sequence represents the Human immunodeficiency virus  
 CC (HIV-1) vpr protein described in the method of the invention. (Updated on  
 CC 12-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 96 AA;  
 Query Match 100.0%; Score 262; DB 3; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEQAPEDQGQPPREPNYNEWTLLELLEKSEAVRHFPRFWLHNLGQHIY 47  
 DB 1 MEQAPEDQGQPPREPNYNEWTLLELLEKSEAVRHFPRFWLHNLGQHIY 47  
 RESULT 7  
 AAB10685  
 ID AAB10685 standard; peptide; 96 AA.  
 AC AAB10685;  
 XX  
 XX 19-JAN-2001 (first entry)  
 DT  
 XX HIV-1 regulatory virus protein R peptide svPr1-96.  
 DE  
 XX Regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity;  
 KW structural analysis; cell cycle arrest.  
 KW  
 XX Synthetic.  
 OS  
 XX Human immunodeficiency virus 1.  
 OS  
 XX WO200049038-A2.  
 PN  
 XX 24-AUG-2000.  
 PD  
 XX

PF 19-FEB-2000; 2000WO-DE000525.  
 XX  
 PR 19-FEB-1999; 99DE-01008752.  
 PR 19-FEB-1999; 99DE-01008766.  
 XX  
 PA (SCHU/) SCHUBERT U.  
 PA (HENK/) HENKLEIN P.  
 PA (WRAY/) WRAY V.  
 XX  
 PI Schubert U, Henklein P, Wray V;  
 XX WPI; 2000-565367/52.  
 DR  
 XX New synthetic peptides from the Vpr protein of human immune deficiency  
 PT virus, useful e.g. for therapy and diagnosis, have good solubility in  
 PT water.  
 PT  
 XX Claim 3.1; Page 5; 35pp; German.  
 PS  
 XX This invention describes novel synthetic peptides (I) derived from the  
 CC regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-  
 CC 1) which have antiviral activity and can be used for gene therapy. (I) is  
 CC used for therapeutic and/or diagnostic purposes, especially in biological  
 CC assays, for development of serological tests or enzyme-linked  
 CC immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in  
 CC blood), to raise specific antibodies and antisera (especially those  
 CC reactive with specific epitopes), and as antiviral agents. (I) can also  
 CC modulate interaction of Vpr with cellular factors, transcription-  
 CC activating properties of Vpr, transport of Vpr and its incorporation into  
 CC viral particles, Vpr-induced cell cycle arrest, and cytotoxic and ion-  
 CC channel activities of Vpr. (I) is used to establish cell or animal  
 CC models for studying pathogenicity of Vpr, for structural analysis of Vpr  
 CC and its domains, for in vitro assembly of new vectors for gene therapy,  
 CC in vitro or in vivo, for complementing the function of Vpr-defect mutants  
 CC in cell cultures, and to reduce flexibility of Vpr induced by the N-  
 CC terminal domain. Synthetic (I), are soluble in water and can be  
 CC formulated as highly concentrated solutions (mmolar) without protein  
 CC aggregation, so are well suited to analysis by nuclear magnetic  
 CC resonance, X-ray or circular dichroism techniques. (I) adopt a folded  
 CC structure, have biological activity comparable to that of viral Vpr, and  
 CC can be produced, at high purity, on the milligram scale. This sequence  
 CC represents the synthetic HIV-1 derived Vpr peptide svPr1-96 which is used  
 CC in the method of the invention  
 XX  
 SQ Sequence 96 AA;  
 Query Match 100.0%; Score 262; DB 3; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEQAPEDQGQPPREPNYNEWTLLELLEKSEAVRHFPRFWLHNLGQHIY 47  
 DB 1 MEQAPEDQGQPPREPNYNEWTLLELLEKSEAVRHFPRFWLHNLGQHIY 47  
 RESULT 8  
 AAE16129  
 ID AAE16129 standard; protein; 96 AA.  
 AC AAE16129;  
 XX  
 XX 29-AUG-2003 (revised)  
 DT  
 XX 26-MAR-2002 (first entry)  
 DT  
 XX Human immunodeficiency virus type 1 (HIV-1) sVpr protein.  
 DE  
 XX Human immunodeficiency virus type 1; HIV-1; auxiliary protein; cancer;  
 KW Vpr protein; regulatory protein; pathogen; cell proliferation; therapy;  
 KW dysregulated cell growth; hyperproliferative cell disorder; malignancy;  
 KW radiation therapy; psoriasis; transgene expression; immune response;  
 KW cytostatic; apoptotic.  
 KW  
 XX

OS Human immunodeficiency virus 1.  
 XX Key Location/Qualifiers  
 XX Region 17..29  
 FT /label= Alpha\_1\_helix  
 FT Region 36..47  
 FT /label= Alpha\_2\_helix  
 FT Region 53..78  
 FT /label= Alpha\_3\_helix  
 XX  
 XX WO200190159-A2.  
 XX  
 XX 29-NOV-2001.  
 XX  
 XX 23-MAY-2001; 2001WO-US016943.  
 XX  
 XX 23-MAY-2000; 2000US-0206610P.  
 PR 09-FEB-2001; 2001US-0267827P.  
 PR 20-APR-2001; 2001US-00839329.  
 XX  
 XX (GLAD-) GLADSTONE INST J DAVID.  
 PA (SCHU/) SCHUBERT U.  
 PA (HENK/) HENKLEIN P.  
 XX  
 XX Schubert U, Henklein P, Sherman MP, Greene WC, De Noronha CMC;  
 XX WPI; 2002-083087/11.  
 XX  
 XX Delivering molecule into cell for inhibiting cell proliferation and  
 PT killing target cell, comprises contacting cell with Vpr polypeptide,  
 PT regulatory protein encoded by HIV type 1, alone or conjugated to  
 PT molecule.  
 XX  
 XX Example 1; Fig 1A; 72pp; English.  
 XX  
 CC The present invention relates to compositions comprising Vpr polypeptides  
 CC conjugated to a therapeutic molecule. Vpr polypeptides are regulatory or  
 CC auxiliary proteins encoded by a lentivirus, human immunodeficiency virus  
 CC type 1 (HIV-1). The invention also relates to a method for delivering a  
 CC molecule into a cell which comprises contacting the cell with a conjugate  
 CC comprising a Vpr polypeptide conjugated to the molecule. The method is  
 CC useful for delivering a polypeptide, polynucleotide (DNA or RNA) or a  
 CC toxin into a cell, preferably a cancer cell, or a cell infected with a  
 CC pathogen such as lentivirus, HIV or retrovirus, bacterium or a parasite.  
 CC Compositions comprising Vpr polypeptide conjugated to a toxin is useful  
 CC for killing a cancer cell or a cell infected with a pathogen where the  
 CC toxin is further conjugated to a regulatory molecule and the contact with  
 CC the target cell exerts an effect on the regulatory molecule that results  
 CC in activation of the toxin. The method is useful for inhibiting cell  
 CC proliferation and treating a disorder associated with dysregulated cell  
 CC growth in a subject. Vpr polypeptides when administered alone are useful  
 CC for increasing sensitivity to radiation therapy in a subject undergoing  
 CC radiation therapy. They can also be used to treat hyperproliferative cell  
 CC disorders such as malignancies, psoriasis and other disorders associated  
 CC with dysregulated cell growth. Vpr polypeptides conjugated to a  
 CC regulatory moiety is useful for modulating the expression of a transgene  
 CC in a cell. Vpr polypeptides alone or conjugated to an antigen is useful  
 CC for increasing an immune response. The present sequence is synthetic Vpr  
 CC (vPr) protein from HIV-1. (Updated on 29-AUG-2003 to standardise OS  
 CC field)  
 XX  
 XX SQ Sequence 96 AA;  
 Query Match 100.0%; Score 262; DB 5; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGHY 47  
 |||||  
 Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGHY 47  
 |||||  
 RESULT 9  
 ADD01277  
 ID ADD01277 standard; protein; 96 AA.

ABP56175  
 ID ABP56175 standard; peptide; 96 AA.  
 XX  
 AC ABP56175;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 28-MAR-2003 (first entry)  
 XX  
 XX HIV-1 viral protein R (Vpr) amino acid sequence.  
 XX  
 KW Mitochondrial membrane permeabilisation; mitochondrion; PTPC;  
 KW permeability transition pore complex; virucide; neuroprotective;  
 KW vasotropic; cytostatic; infection; cell death regulation; apoptosis;  
 KW mitochondrial permeability transition pore complex modulator; cancer;  
 KW apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 XX WO200261105-A2.  
 XX  
 XX 08-AUG-2002.  
 XX  
 XX 01-FEB-2002; 2002WO-EF001633.  
 PF  
 XX 02-FEB-2001; 2001US-0265594P.  
 XX  
 XX (INSP ) INST PASTEUR.  
 XX (CNRS ) CENT NAT RECH SCI.  
 XX  
 XX Edelman L, Jacotot E, Briand J;  
 PI  
 XX WPI; 2002-619260/66.  
 XX  
 XX New chimeric bifunctional molecules that target specific cells and  
 PT regulate the apoptosis function of the permeability transition pore  
 PT complex of the mitochondria, useful for treating or preventing e.g.  
 PT cancer or ischemia.  
 XX  
 XX Disclosure; Page 13; 76pp; English.  
 XX  
 CC The present invention describes a chimeric bifunctional molecule (I)  
 CC comprising at least a first functional molecule covalently linked to a  
 CC second functional molecule, which is able to modulate the activity of the  
 CC permeability transition pore complex (PTPC) of the mitochondria. (I) has  
 CC the function of specifically targeting and entering a tissue cell  
 CC population. The second functional molecule has the function of  
 CC specifically targeting, and inducing or preventing the death of the cells  
 CC by apoptosis by regulating the opening or the closing of the PTPC of the  
 CC mitochondria or its fragment. (I) has virucide, neuroprotective,  
 CC vasotropic and cytostatic activities, and can be used as a mitochondrial  
 CC permeability transition pore complex (PTPC) modulator. (I) is useful for  
 CC treating or preventing a pathological infection or disease. (I) is also  
 CC useful for regulating cell death regulatory molecules, specifically the  
 CC apoptogenic function of the PTPC, for treating e.g. cancer, ischaemia,  
 CC neurodegenerative diseases, fulminant hepatitis or viral infections. The  
 CC present sequence represents the HIV-1 viral protein R (Vpr) amino acid  
 CC sequence, which is given in the exemplification of the present invention.  
 CC (Updated on 29-AUG-2003 to standardise OS field)  
 XX  
 XX SQ Sequence 96 AA;  
 Query Match 100.0%; Score 262; DB 5; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGHY 47  
 |||||  
 Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGHY 47  
 |||||  
 RESULT 10  
 ADD01277  
 ID ADD01277 standard; protein; 96 AA.

XX ADD01277;  
 AC 01-JAN-2004 (first entry)  
 DT HIV-1 Vpr CyPA protein binding motif.  
 DE  
 XX lentivirus protein R; Vpr; inhibitor; cellular chaperone; folding;  
 KW stability; cyclophilin A; CyPA; cell-cycle arrest; apoptosis;  
 KW glucocorticoid receptor coactivation; anti-HIV; neurotropic; nephrotropic;  
 KW antileptic; antiretroviral; AIDS; infection; HIV-induced dementia;  
 KW lipodystrophy syndrome; lipid metabolism; HIV-associated nephropathy.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 XX WO2003038032-A2.  
 PN  
 XX 08-MAY-2003.  
 PD  
 XX 25-OCT-2002; 2002WO-DE004052.  
 PF  
 XX 25-OCT-2001; 2001DE-01053902.  
 PR  
 XX (MEDI-) MEDICIS VENTURES MANAGEMENT GMBH.  
 PA  
 XX Will H, Tessmer U, Bruns K;  
 PI WPI; 2003-430506/40.  
 DR  
 XX Agent for inhibiting lentivirus Vpr protein, useful for treatment and  
 PT prevention of infection by human immune deficiency virus, is inhibitor of  
 PT chaperone enzyme.  
 PT  
 XX Disclosure; Fig 4; 41pp; German.  
 XX  
 CC This invention describes a novel agent (A), for inhibiting the primate  
 CC lentivirus protein R (Vpr) of HIV-1 or -2, or simian immune deficiency  
 CC virus, comprising an inhibitor (I) of cellular chaperones (II) that are  
 CC essential for proper folding, stability and, thus, biological function of  
 CC Vpr. The inhibitor is useful for inhibiting interaction of Vpr with  
 CC cyclophilins include cyclosporin A, FK506, rapamycin and the non-  
 CC immunosuppressive compounds SDZ NIM811 and/or sangliferin A. Vpr first  
 CC binds to cyclophilin A (CyPA) to regulate the trans conformation of  
 CC proline peptidyl bonds in the N-terminus of Vpr. The inhibitor prevents  
 CC cis-trans rearrangement, specifically of pro residues at positions 5, 10,  
 CC 14 and 35 of Vpr. The inhibitor may also act by a process in which CyPA  
 CC co-translationally regulates expression, folding and stability of Vpr and  
 CC this stabilizing process is active in cells transfected with the  
 CC specified viruses, with DNA that encodes Vpr, or with recombinant Vpr-  
 CC encoding retro, adeno, vaccinia or baculo viruses. All essential  
 CC functions of Vpr (induction of cell-cycle arrest, apoptosis, increased  
 CC viral production and co-activation of glucocorticoid receptors) are  
 CC inhibited. The products of the invention have anti-HIV, neurotropic,  
 CC nephrotropic and antileptic activity. The inhibitor may be used in  
 CC combination with other antiretroviral agents; blockers of reverse  
 CC transcription and/or protease; genetically based antiretroviral  
 CC therapies, intracellular immunization and administration of anti-HIV gene  
 CC in stem cells and/or peripheral CD4+ lymphocytes, especially in advanced  
 CC stages of disease. The agent of the invention is used to prevent and  
 CC treat lentiviral infections, specifically AIDS or HIV infections  
 CC (including where asymptomatic), also HIV-induced dementia (by inhibiting  
 CC infection of neurons, glial cells and endothelial cells in cerebral  
 CC capillaries). HIV-associated lipodystrophy syndrome or other disorders of  
 CC lipid metabolism and HIV-associated nephropathy, also to prevent systemic  
 CC infection immediately after exposure to HIV, e.g. needle pricks with HIV-  
 CC contaminated blood. This sequence represents the CyPA binding fragment at  
 CC the N-terminal of the HIV-1 (NL4-3) Vpr protein.  
 XX  
 XX Sequence 96 AA;

Query Match 100.0%; Score 262; DB 7; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRIMLHNLGQHIY 47  
 DB 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRIMLHNLGQHIY 47

RESULT 11  
 ADF46812  
 ID ADF46812 standard; protein; 96 AA.  
 XX  
 AC ADF46812;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE HIV-1 Vpr protein.  
 XX  
 KW virus protein R; Vpr; functional analysis.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN JP2003259881-A.  
 XX  
 PD 16-SEP-2003.  
 PF  
 XX 12-MAR-2002; 2002JP-00066938.  
 PR  
 XX 12-MAR-2002; 2002JP-00066938.  
 PA (ORIY) ORIENTAL YEAST CO LTD.  
 XX (NAKA/) NAKAMURA T.  
 DR WPI; 2004-026590/03.  
 DR N-PSDB; ADF46813.  
 XX

PT Producing recombinant virus protein R (Vpr), useful in promoting  
 PT immunodeficiency virus reproduction, involves transforming a host cell  
 PT with an expression vector for the protein.  
 PS Claim 1; SEQ ID NO 1; 14pp; Japanese.  
 XX  
 CC The invention relates to a method of producing a recombinant HIV-1 virus  
 CC protein R (Vpr) protein or a protein having one or more substitutions,  
 CC additions or alterations and having biological activity, by transforming  
 CC a host Escherichia coli cell with an expression vector containing the  
 CC gene encoding Vpr, and culturing the transformed cell. The method is  
 CC useful for producing recombinant Vpr protein. The protein is useful for  
 CC promoting the reproduction of immunodeficiency virus in cell, tissue or  
 CC organ derived from an organism. The protein is useful for functional  
 CC analysis of the Vpr protein. This sequence represents the HIV-1 Vpr  
 CC protein.  
 XX  
 SQ Sequence 96 AA;

Query Match 100.0%; Score 262; DB 8; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRIMLHNLGQHIY 47  
 DB 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRIMLHNLGQHIY 47

RESULT 12  
 ABM79669  
 ID ABM79669 standard; protein; 96 AA.  
 XX  
 AC ABM79669;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE HIV-1 Vpr protein.  
 XX  
 KW HIV; Vpr; modulator; anti-HIV; virucide.

XX OS Human immunodeficiency virus type 1.  
 XX PN WO2003076621-A2.  
 XX PD 18-SEP-2003.  
 XX XX 07-MAR-2003; 2003WO-CA000325.  
 XX PF 08-MAR-2002; 2002US-0362384P.  
 XX PR (UIMO-) UNIV MONTREAL.  
 XX PA Cohen EA, Yao X, Belhumeur P, Lemay J;  
 XX PI WPI; 2004-042337/04.  
 XX DR  
 XX XX New polypeptides that bind to viral Vpr protein, useful for treatment,  
 PT prevention, diagnosis and prognosis of immune deficiency virus infection.  
 XX XX  
 XX PS Example 20; Page 33-34; 143pp; English.  
 XX CC The present invention relates to peptide which are capable of binding to  
 CC the HIV protein vpr and/or modulates vpr-related activity. Such peptides  
 CC are used for prevention, treatment, diagnosis and prognosis of vpr-  
 CC related diseases, particularly lentiviral infection (specifically HIV-1  
 CC or -2, or simian immune deficiency virus), for modulating, particularly  
 CC inhibiting, vpr-related activities and for detecting vpr in a sample.  
 CC Nucleic acids encoding such peptides and cells that contain this nucleic  
 CC acid can also be used therapeutically. The present sequence is a protein  
 CC of relevance to the invention  
 XX CC  
 XX SQ Sequence 96 AA;  
 Query Match 100.0%; Score 262; DB 8; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEQAPEDQGPQRPYNWTLLEELKSEAVRHPRIWLHNLGQHIY 47  
 DB 1 MEQAPEDQGPQRPYNWTLLEELKSEAVRHPRIWLHNLGQHIY 47  
 RESULT 13  
 ABR55491  
 ID ABR55491 standard; protein; 96 AA.  
 XX AC ABR55491;  
 XX DT 11-AUG-2003 (first entry)  
 XX DE Amino acid sequence of a HIV vpr protein.  
 XX KW Polymorphic marker; host response; HIV; AIDS related virus; vaccine;  
 KW hepatitis related virus; HCV; HBV; drug resistance; vpr.  
 XX OS Human immunodeficiency virus.  
 XX PN WO2003035097-A1.  
 XX PD 01-MAY-2003.  
 XX PF 23-OCT-2002; 2002WO-AU001450.  
 XX PR 23-OCT-2001; 2001AU-00008425.  
 XX PA (EPIP-) EPIPOT PTY LTD.  
 XX PI Mallal S;  
 XX DR WPI; 2003-449231/42.  
 XX PT Determining the influence of variation in host genes on the selection of

PT microorganisms with protein substitutions, comprises typing individuals  
 PT of a cohort infected with a microorganism for an intrinsic polymorphic  
 XX marker.  
 XX PS Claim 22; Page 89; 157pp; English.  
 XX CC The specification describes a method of determining the influence of  
 CC variation in host genes on selection of microorganisms with protein  
 CC substitutions. The method comprises typing all individuals of a  
 CC population of patients infected with a microorganism for at least one  
 CC selected intrinsic polymorphic marker involved in the host response to  
 CC the presence of the microorganism. The method is useful for examining  
 CC selective pressures confronting a wide range of organisms that exhibit  
 CC pathogenic traits in a host, such as bacteria, fungi, mycobacterium,  
 CC viruses and virus-like particles; for examining microorganisms that have  
 CC adapted to evolve rapidly, including HIV and AIDS related viruses and the  
 CC hepatitis related viruses such as HCV and HBV. The method is useful for  
 CC designing a vaccine to prevent or delay the emergence of drug resistance  
 CC in patients treated with a particular drug specific for a microorganism  
 CC where the drug affects the replication of the microorganism at the  
 CC nucleotide or amino acid level. The present sequence represents a HIV vpr  
 CC protein, which is expected to provide optimal cytotoxic T lymphocyte  
 CC (CTL) induced therapeutic protection to the cohort examined in that study  
 XX CC  
 XX SQ Sequence 96 AA;  
 Query Match 97.7%; Score 256; DB 6; Length 96;  
 Best Local Similarity 97.9%; Pred. No. 3.9e-25;  
 Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MEQAPEDQGPQRPYNWTLLEELKSEAVRHPRIWLHNLGQHIY 47  
 DB 1 MEQAPEDQGPQRPYNWTLLEELKSEAVRHPRIWLHNLGQHIY 47  
 RESULT 14  
 AAB69306  
 ID AAB69306 standard; protein; 96 AA.  
 XX AC AAB69306;  
 XX DT 12-SEP-2003 (revised)  
 DT 20-APR-2001 (first entry)  
 XX DE HIV-1 non-subtype B clone 93BR029-4 vpr protein.  
 XX KW HIV-1; human immunodeficiency virus; non-subtype B; gag; pol; env; vpu;  
 KW vif; vpr; tat; rev; nef; vaccine.  
 XX OS Human immunodeficiency virus 1.  
 XX PN WO200026416-A1.  
 XX PD 11-MAY-2000.  
 XX PF 25-OCT-1999; 99WO-US024837.  
 XX PR 02-NOV-1998; 98US-00184418.  
 XX PA (UABR-) UAB RES FOUND.  
 XX PI Hahn BH, Shaw GM, Gao F;  
 XX DR WPI; 2000-365651/31.  
 XX PT Novel genomic nucleic acids of non-subtype B human immunodeficiency virus  
 PT type 1 useful for detecting and treating AIDS comprises a specific  
 PT nucleotide sequence.  
 XX PS Claim 41; Fig 17; 131pp; English.  
 XX CC The present invention provides the protein and coding sequences for a  
 CC number of human immunodeficiency virus (HIV) type 1 non-subtype B

CC isolates. The sequences shown include the near full-length coding  
 CC sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat,  
 CC rev and nef proteins. These can be used to detect the presence of HIV-1  
 CC in a sample and to produce antibodies against non-subtype B HIV-1 virus.  
 CC These antibodies can be used in vaccines to prevent and treat HIV  
 CC infection. (Updated on 12-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 96 AA;

Query Match 97.3%; Score 255; DB 3; Length 96;  
 Best Local Similarity 95.7%; Pred. NO. 5.3e-25;  
 Matches 45; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHFPRIWLNHGQHIY 47  
 |||||  
 DB 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHFPRLWLSLQHIY 47  
 |||||

## RESULT 15

AAU80187  
 ID AAU80187 standard; protein; 96 AA.

XX  
 AC AAU80187;

XX  
 DT 29-AUG-2003 (revised)

XX  
 DT 15-JUL-2002 (first entry)

XX  
 DE HIV-1 Vpr protein.

XX  
 KW HIV-1; acquired immunodeficiency syndrome; AIDS; Vpr.

XX  
 OS Human immunodeficiency virus 1.

XX  
 FH Key Location/Qualifiers

XX  
 FT Misc-difference 45 /note= "Encoded by CAT"

XX  
 FT  
 XX  
 PN JP2002085099-A.

XX  
 PD 26-MAR-2002.

XX  
 PF 14-SEP-2000; 2000JP-00280851.

XX  
 PR 14-SEP-2000; 2000JP-00280851.

XX  
 PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.

XX  
 PA (ORIY ) ORIENTAL YEAST CO LTD.

XX  
 DR WPI; 2002-378279/41.

XX  
 DR N-PSDB; ABK50386.

XX  
 PT Detection of immunodeficiency virus by detecting the presence of Vpr  
 protein.

XX  
 PS Disclosure; Page 8; 17pp; Japanese.

XX  
 CC The invention relates to a method for detecting immunodeficiency virus in  
 CC a sample in which the presence of Vpr (not defined) protein in the sample  
 CC is detected. Also included are a kit for use in the above detecting  
 CC method containing a cell and a pigment, and a method for screening a  
 CC compound promoting or inhibiting the intake of a substance having a  
 CC molecular weight (M.W.) of 300 to 3000 in which the promotion or the  
 CC inhibition of intake of the substance by the presence of a test compound  
 CC is used as the index in the intake of the substance to the cell by a  
 CC treatment using a sample containing Vpr protein. The method is used for  
 CC detecting immunodeficiency virus (e.g. Human immunodeficiency virus-1,  
 CC the causative agent of acquired immunodeficiency virus syndrome, AIDS) in  
 CC a sample. The present sequence represents HIV-1 Vpr. (Updated on 29-AUG-  
 CC 2003 to standardise OS field)

XX  
 SQ Sequence 96 AA;

Query Match 96.2%; Score 252; DB 5; Length 96;

Best Local Similarity 97.9%; Pred. NO. 1.3e-24;  
 Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHFPRIWLNHGQHIY 47  
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 DB 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHFPRIWLNHGQMIY 47  
 |||||

Search completed: October 18, 2004, 18:45:32  
 Job time : 63.6875 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:42:45 ; Search time 27.4167 Seconds  
(without alignments)  
113.688 Million cell updates/sec

Title: US-09-913-927D-2  
 Perfect score: 262  
 Sequence: 1 MEAPEDOGPOREPYNEWTL,.....SEAVRHEPRIVHNLGSHY 47

Scoring table: BLOSUM62  
Gap: 10.0    Gapext: 0.5

Searched: 478139 seas. 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 entries

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5: /cgn2_6/pdata/1/iaa/pRTUS COMB pep.*
6: /cgn2_6/pdata/1/iaa/backfiles1 pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	262	100.0	96	4	US-09-309-572-19	Sequence 19, Appl
2	262	100.0	96	4	US-09-718-096-19	Sequence 19, Appl
3	252	96.2	96	3	US-08-704-856C-15	Sequence 15, Appl
4	252	96.2	96	4	US-09-242-881-15	Sequence 15, Appl
5	249	95.0	96	4	US-09-839-329-1	Sequence 1, Appl
6	248	94.7	72	2	US-08-301-915-4	Sequence 4, Appl
7	248	94.7	72	3	US-08-524-694A-4	Sequence 4, Appl
8	248	94.7	72	4	US-09-454-156A-4	Sequence 4, Appl
9	248	94.7	78	3	US-09-124-900-5	Sequence 5, Appl
10	248	94.7	96	2	US-08-301-915-1	Sequence 1, Appl
11	248	94.7	96	3	US-08-524-694A-1	Sequence 1, Appl
12	248	94.7	96	4	US-09-454-156A-1	Sequence 1, Appl
13	238	90.8	95	4	US-09-319-588C-10	Sequence 10, Appl
14	220	84.0	100	4	US-09-463-917A-116	Sequence 116, App
15	209	79.8	100	4	US-09-462-917A-115	Sequence 115, App
16	206	78.6	93	4	US-09-462-917A-117	Sequence 117, App
17	194	74.0	100	4	US-09-462-917A-118	Sequence 118, App
18	138	52.7	100	4	US-09-208-551-49	Sequence 49, Appl
19	118	45.0	3077	6	5223423-2	Patent No. 5223423
20	111	42.4	105	2	US-08-301-915-2	Sequence 2, Appl
21	111	42.4	105	3	US-08-524-694A-2	Sequence 2, Appl
22	111	42.4	105	4	US-09-454-156A-2	Sequence 2, Appl
23	110	42.0	20	3	US-09-055-075C-8	Sequence 8, Appl
24	110	42.0	20	4	US-09-519-124-8	Sequence 8, Appl
25	110	42.0	21	5	PCT-US994-02191-4	Sequence 4, Appl
26	103	39.3	105	2	US-08-659-251-9	Sequence 9, Appl
27	103	39.3	105	3	US-09-256-490-9	Sequence 9, Appl

28	103	39.3	105	5	PCT-US96-11445-9	Sequence 9, Appl
29	90	34.4	17	3	US-09-055-075C-10	Sequence 10, Appl
30	90	34.4	17	3	US-09-055-075C-12	Sequence 12, Appl
31	90	34.4	17	4	US-09-919-114-10	Sequence 10, Appl
32	90	34.4	17	4	US-09-919-114-12	Sequence 12, Appl
33	78	28.8	13	2	US-08-188-583-33	Sequence 33, Appl
34	77	29.4	14	2	US-08-484-905-56	Sequence 56, Appl
35	77	29.4	14	3	US-08-481-985B-56	Sequence 56, Appl
36	77	29.4	14	3	US-08-370-476-56	Sequence 56, Appl
37	68	26.0	12	5	PCT-US94-02191-5	Sequence 5, Appl
38	68	26.0	12	5	PCT-US94-02191-8	Sequence 8, Appl
39	68	26.0	14	3	US-08-992-877-36	Sequence 36, Appl
40	64	24.4	508	2	US-08-724-281-1	Sequence 1, Appl
41	64	24.4	508	4	US-09-134-377-1	Sequence 1, Appl
42	61	23.3	335	4	US-09-270-767-60286	Sequence 60286, A
43	61	23.3	355	4	US-09-270-767-44816	Sequence 44816, A
44	59.5	22.7	3165	2	US-08-459-146-3	Sequence 3, Appl
45	59.5	22.7	3165	2	US-08-459-065-3	Sequence 3, Appl

## ALIGNMENTS

```

RESULT 1
US-09-309-572-19
; Sequence 19, Application US/09309572
; Patent No. 6440730
; GENERAL INFORMATION:
; APPLICANT: Heinrich-Pette-Institut
; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
; FILE REFERENCE: P50489
; CURRENT APPLICATION NUMBER: US/09/309,572
; CURRENT FILING DATE: 1999-05-11
; EARLIER APPLICATION NUMBER: DE 198 56 463
; EARLIER FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: vpr protein
US-09-309-572-19

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	Query Match	100.0%;	Score 262;	DB 4;	Length 96;
	Best Local Similarity	100.0%;	Pred. No. 1.8e-27;		
	Matches 47;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MEQAPEDQGPQPEYNEWTELEELKSEAVRHFPRWLHNLGQHIY	47		
Dh	1	MEQAPEDQGPQPEYNEWTELEELKSEAVRHFPRWLHNLGQHIY	47		

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RESULT 2
US-09-718-096-19
/ Sequence 19, Application US/09718096
/ Patent No. 6589763
/ GENERAL INFORMATION:
/ APPLICANT: Von Laer, Meike-Dorothee
/ TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
/ FILE REFERENCE: 35-195
/ CURRENT APPLICATION NUMBER: US/09/718,096
/ CURRENT FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: DE 19856463.5
/ PRIOR FILING DATE: 1998-11-26
/ PRIOR APPLICATION NUMBER: EP 99250415.9
/ PRIOR FILING DATE: 1999-11-25
/ PRIOR APPLICATION NUMBER: US 09/309,572
/ PRIOR FILING DATE: 1999-05-11
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 19

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; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: vpr protein
US-09-718-096-19

Query Match      100.0%; Score 262; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.8e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47
   |||||
Db 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 3
US-08-704-856C-15
; Sequence 15, Application US/08704856C
; Patent No. 6042832
; GENERAL INFORMATION:
; APPLICANT: Koprowski, Hilary
; APPLICANT: Yusibov, Vidadi
; APPLICANT: Hooper, Douglas, C.
; APPLICANT: Modelska, Anna
; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allan H. Fried & Associates
; STREET: 1525 Locust Street, 15th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Corel WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,856C
; FILING DATE: 28-Aug-1996
; CLASSIFICATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: N
; APPLICATION NUMBER: US/08/704,856C
; FILING DATE: 28-Aug-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: N
; APPLICATION NUMBER: US/08/704-856C-15

Query Match      96.2%; Score 252; DB 3; Length 96;
Best Local Similarity 95.7%; Pred. No. 3.9e-26;
Matches 45; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47
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Db 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 4
US-09-242-881-15
; Sequence 15, Application US/09242881
; Patent No. 6448070
; GENERAL INFORMATION:
; APPLICANT: Koprowski, Hilary
; APPLICANT: Yusibov, Vidadi
; APPLICANT: Hooper, Douglas, C.
; APPLICANT: Modelska, Anna
; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allan H. Fried & Associates
; STREET: 1525 Locust Street, 15th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Corel WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/242,881
; FILING DATE: 25-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,856
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: N
; APPLICATION NUMBER: US/09/242-881-15

Query Match      96.2%; Score 252; DB 4; Length 96;
Best Local Similarity 95.7%; Pred. No. 3.9e-26;
Matches 45; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47
   |||||
Db 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 5
US-09-839-329-1
; Sequence 1, Application US/09839329
; Patent No. 6664040
; GENERAL INFORMATION:
; APPLICANT: Michael P. Sherman
; APPLICANT: Warner C. Greene
; APPLICANT: Carlos M.C. de No. 6664040ohna
; APPLICANT: Ulrich Schubert
; APPLICANT: Peter Henklein
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF
; FILE REFERENCE: G&C 30448.91-US-U2
; CURRENT APPLICATION NUMBER: US/09/839,329
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/206,610
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/267,827
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide of regulatory virus proteins R
; OTHER INFORMATION: (vpr) of human immunodeficiency virus type 1
; OTHER INFORMATION: (HIV-1)
US-09-839-329-1

Query Match          95.0%; Score 249; DB 4; Length 96;
Best Local Similarity 97.9%; Pred. No. 9.7e-26;
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEQAPDQGPQREPYNEWTLLELLEKSEAVRHPRIWLHNLGQHIY 47
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Db 1 MEQAPDQGPQREPYNEWTLLELLEKSEAVRHPRIWLHNLGQHIY 47

RESULT 6
US-08-301-915-4
; Sequence 4, Application US/08301915
; Patent No. 5861161
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS
; TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301.915
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-301-915-4

Query Match          94.7%; Score 248; DB 2; Length 72;
Best Local Similarity 93.6%; Pred. No. 9.3e-26;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEQAPDQGPQREPYNEWTLLELLEKSEAVRHPRIWLHNLGQHIY 47
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Db 1 MEQAPDQGPQREPYNEWTLLELLEKSEAVRHPRIWLHNLGQHIY 47

RESULT 7
US-08-524-694A-4
; Sequence 4, Application US/08524694A
; Patent No. 6043081
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS
; TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524.694A
; FILING DATE: September 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-524-694A-4

Query Match          94.7%; Score 248; DB 3; Length 72;
Best Local Similarity 93.6%; Pred. No. 9.3e-26;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEQAPDQGPQREPYNEWTLLELLEKSEAVRHPRIWLHNLGQHIY 47
|||||
Db 1 MEQAPDQGPQREPYNEWTLLELLEKSEAVRHPRIWLHNLGQHIY 47

RESULT 8
US-09-454-156A-4
; Sequence 4, Application US/09454156A
; Patent No. 6468539
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS
; TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
```

;; COUNTRY: U.S.A.  
;; ZIP: 07601  
;; COMPUTER READABLE FORM: disk  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/454,156A  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/301,915  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: JACKSON, David A.  
;; REGISTRATION NUMBER: 26,742  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-487-5800  
;; TELEFAX: 201-343-1684  
;; TELEX: 133521  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 72 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
US-09-454-156A-4

Query Match 94.7%; Score 248; DB 4; Length 72;  
Best Local Similarity 93.6%; Pred. No. 9.3e-26;  
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNYNEWTLLELELKSEAVRHFPRFWLHNLGQHIY 47  
Db 1 MEQAPEDQGPQREPNYNEWTLLELELKSEAVRHFPRFWLHNLGQHIY 47

RESULT 9  
US-09-124-900-5  
; Sequence 5, Application US/09124900  
; Patent No. 6268484  
; GENERAL INFORMATION:  
; APPLICANT: KATINGER, Hermann  
; APPLICANT: BUCHACHER, Andrea  
; APPLICANT: ERNST, Wolfgang  
; APPLICANT: BALLAUN, Claudia  
; APPLICANT: PURTSCHER, Martin  
; APPLICANT: TRKOLA, Alexandra  
; APPLICANT: FREDL, Renate  
; APPLICANT: SCHMATZ, Christine  
; APPLICANT: KLIMA, Annelies  
; APPLICANT: STEINDL, Franz  
; APPLICANT: MUSTER, Thomas  
; TITLE OF INVENTION: HIV-Vaccines  
; FILE REFERENCE: 1939-112P  
; CURRENT APPLICATION NUMBER: US/09/124,900  
; PRIOR FILING DATE: 1998-07-30  
; PRIOR APPLICATION NUMBER: PCT/EP95/01481  
; PRIOR FILING DATE: 1995-04-19  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 78  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-124-900-5

Query Match 94.7%; Score 248; DB 3; Length 78;  
Best Local Similarity 93.6%; Pred. No. 1e-25;  
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNYNEWTLLELELKSEAVRHFPRFWLHNLGQHIY 47  
Db 1 MEQAPEDQGPQREPNYNEWTLLELELKSEAVRHFPRFWLHNLGQHIY 47

RESULT 10  
US-08-301-915-1  
; Sequence 1, Application US/08301915  
; Patent No. 5861161  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, Eric A.  
; APPLICANT: BERGERON, Dominique  
; APPLICANT: CHECROUNE, Florent  
; APPLICANT: YAO, Xiao-Jian  
; APPLICANT: PIGNAC-KOBINGER, Gary  
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS  
; TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KLAUBER & JACKSON  
; STREET: Continental Plaza, 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: N.J.  
; COUNTRY: U.S.A.  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/301,915  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: JACKSON, David A.  
; REGISTRATION NUMBER: 26,742  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 96 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-301-915-1

Query Match 94.7%; Score 248; DB 2; Length 96;  
Best Local Similarity 93.6%; Pred. No. 1.3e-25;  
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNYNEWTLLELELKSEAVRHFPRFWLHNLGQHIY 47  
Db 1 MEQAPEDQGPQREPNYNEWTLLELELKSEAVRHFPRFWLHNLGQHIY 47

RESULT 11  
US-08-524-694A-1  
; Sequence 1, Application US/08524694A  
; Patent No. 6043081  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, Eric A.  
; APPLICANT: BERGERON, Dominique  
; APPLICANT: CHECROUNE, Florent  
; APPLICANT: YAO, Xiao-Jian  
; APPLICANT: PIGNAC-KOBINGER, Gary  
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED  
; TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES



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; TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof
; FILE REFERENCE: INNS:014 11362.0014.NPUS00
; CURRENT APPLICATION NUMBER: US/09/462,917A
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: PCT/EP98/04522
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Human
US-09-462-917A-116
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Query Match      84.0%; Score 220; DB 4; Length 100;
Best Local Similarity 85.1%; Pred. No. 7.4e-22;
Matches 40; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNYNTLELLELKSEAVRHFPRWLHNLGQHIY 47
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Db 1 MEQAPEDQGPAREPFNEWTLELLELKAEAVRHFPRWLQALGQIY 47
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RESULT 15
US-09-462-917A-115
; Sequence 115, Application US/09462917A
; Patent No. 6511801
; GENERAL INFORMATION:
; APPLICANT: Delaporte, Eric
; APPLICANT: Peeters, Martine
; APPLICANT: Saman, Eric
; APPLICANT: Vanden Haesevelde, Marlen
; TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof
; FILE REFERENCE: INNS:014 11362.0014.NPUS00
; CURRENT APPLICATION NUMBER: US/09/462,917A
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: PCT/EP98/04522
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Human
US-09-462-917A-115
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Best Local Similarity 78.7%; Pred. No. 2.2e-20;
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QY 1 MEQAPEDQGPQREPNYNTLELLELKSEAVRHFPRWLHNLGQHIY 47
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Db 1 MERAPEDQGPAREPFNEWALELLELKAEAVRHFPRWLQALGQIY 47
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Job time : 28.4167 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:43:30 ; Search time 85.1875 Seconds  
(without alignments)  
178.383 Million cell updates/sec

Title: US-09-913-927D-2  
Perfect score: 262  
Sequence: 1 MEQAPEDQGPQREPNYEWTL.....SEAVRHPRFWLHNLGQHIY 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pap.\*  
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19: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	262	100.0	96	14	US-10-059-261-272
2	249	95.0	96	9	US-09-839-329-1
3	248	94.7	78	14	US-10-283-618-15
4	248	94.7	96	14	US-10-190-435-284
5	244	93.1	96	14	US-10-190-435-276
6	240	91.6	96	14	US-10-190-435-264
7	240	91.6	96	14	US-10-190-435-265
8	240	91.6	96	14	US-10-190-435-266
9	240	91.6	96	14	US-10-190-435-282
10	240	91.6	96	14	US-10-190-435-283
11	240	91.6	96	15	US-10-296-734-4
12	240	91.6	96	15	US-10-296-734-1475
13	239	91.2	96	14	US-10-190-435-258
14	239	91.2	96	14	US-10-190-435-259

15	239	91.2	96	14	US-10-190-435-273	Sequence 273, App
16	238	90.8	95	14	US-10-301-661A-10	Sequence 10, Appl
17	238	90.8	96	14	US-10-190-435-262	Sequence 262, App
18	237	90.5	96	14	US-10-190-435-254	Sequence 254, App
19	237	90.5	96	14	US-10-190-435-285	Sequence 285, App
20	237	90.5	96	14	US-10-190-435-278	Sequence 278, App
21	236	90.1	96	14	US-10-190-435-263	Sequence 263, App
22	235	89.7	96	14	US-10-190-435-256	Sequence 256, App
23	235	89.7	96	14	US-10-190-435-257	Sequence 257, App
24	234	89.3	96	14	US-10-469-199-2	Sequence 2, Appl
25	234	89.3	362	15	US-10-190-435-260	Sequence 260, App
26	233	88.9	96	14	US-10-190-435-261	Sequence 261, App
27	233	88.9	96	14	US-10-190-435-274	Sequence 274, App
28	233	88.9	96	14	US-10-190-435-277	Sequence 277, App
29	233	88.9	96	16	US-10-325-468-36	Sequence 36, Appl
30	233	88.9	96	14	US-10-190-435-268	Sequence 268, App
31	232	88.5	96	14	US-10-190-435-269	Sequence 269, App
32	232	88.5	96	14	US-10-190-435-279	Sequence 279, App
33	230	87.8	96	14	US-10-325-468-11	Sequence 11, Appl
34	229	87.4	96	16	US-10-190-435-267	Sequence 267, App
35	229	87.4	96	14	US-10-296-734-1477	Sequence 1477, Ap
36	227	86.6	96	14	US-10-190-435-270	Sequence 270, App
37	226	86.3	94	15	US-10-190-435-271	Sequence 271, App
38	225	85.9	96	14	US-10-190-435-280	Sequence 280, App
39	225	85.9	96	14	US-09-971-980-63	Sequence 63, Appl
40	222	84.7	96	9	US-10-320-786-116	Sequence 116, App
41	220	84.0	100	14	US-10-190-435-281	Sequence 281, App
42	220	84.0	96	14	US-10-190-435-272	Sequence 272, App
43	219	83.6	96	14	US-10-320-786-115	Sequence 115, App
44	216	82.4	96	14		
45	209	79.8	100	14		

ALIGNMENTS

RESULT 1

US-10-059-261-272  
; Sequence 272, Application US/10059261  
; Publication No. US2003007826A1  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS  
; APPLICANT: BRIAND, JEAN-PAUL  
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC TRANSITION OF THE PERMEABILITY TRANSITION PORE COMPLEX  
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX  
; TITLE OF INVENTION: (PTPC)  
; FILE REFERENCE: 03495.0216  
; CURRENT APPLICATION NUMBER: US/10/059,261  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/265,594  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 325  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 272  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-10-059-261-272

Query Match 100.0%; Score 262; DB 14; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.1e-24;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPNYEWTLLELELKSEAVRHPRFWLHNLGQHIY 47  
Db 1 MEQAPEDQGPQREPNYEWTLLELELKSEAVRHPRFWLHNLGQHIY 47

RESULT 2

US-09-839-329-1  
; Sequence 1, Application US/09839329

```
; Publication No. US20020022027A1
; GENERAL INFORMATION:
; APPLICANT: Michael P. Sherman
; APPLICANT: Warner C. Greene
; APPLICANT: Carlos M.C. de No. 6664040ohna
; APPLICANT: Ulrich Schubert
; APPLICANT: Peter Henklein
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF
; TITLE OF INVENTION: A MOLECULE INTO A CELL
; FILE REFERENCE: G&C 30448-91-US-02
; CURRENT APPLICATION NUMBER: US/09/839,329
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/206,610
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/267,827
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide of regulatory virus proteins R
; OTHER INFORMATION: (vpr) of human immunodeficiency virus type 1
; OTHER INFORMATION: (HIV-1)
US-09-839-329-1

Query Match          95.0%; Score 249; DB 9; Length 96;
Best Local Similarity 97.9%; Pred. No. 8.2e-23;
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHPRIWHLNGLGQHIY 47
Db 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHPRIWHLNGLGQHIY 47

RESULT 3
US-10-283-618-15
; Sequence 15, Application US/10283618
; Publication No. US20030165517A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; APPLICANT: Walker, Bruce
; TITLE OF INVENTION: THERAPEUTIC ANTI-HIV (vpr) COMPOUNDS
; FILE REFERENCE: G2 2111.00
; CURRENT APPLICATION NUMBER: US/10/283,618
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/345,957
; PRIOR FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-10-283-618-15

Query Match          94.7%; Score 248; DB 14; Length 78;
Best Local Similarity 93.6%; Pred. No. 8.6e-23;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHPRIWHLNGLGQHIY 47
Db 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHPRIWHLNGLGQHIY 47

RESULT 4
US-10-190-435-284
; Sequence 284, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
US-10-190-435-284
```

```
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr HXB2
US-10-190-435-284

Query Match          94.7%; Score 248; DB 14; Length 96;
Best Local Similarity 93.6%; Pred. No. 1.1e-22;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHPRIWHLNGLGQHIY 47
Db 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHPRIWHLNGLGQHIY 47

RESULT 5
US-10-190-435-276
; Sequence 276, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 276
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr 92BR025
US-10-190-435-276

Query Match          93.1%; Score 244; DB 14; Length 96;
Best Local Similarity 93.6%; Pred. No. 3.4e-22;
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHPRIWHLNGLGQHIY 47
Db 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHPRIWHLNGLGQHIY 47

RESULT 6
US-10-190-435-264
; Sequence 264, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
```





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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr C2220-Eth
US-10-190-435-283

Query Match          91.6%; Score 240; DB 14; Length 96;
Best Local Similarity 91.5%; Pred. No. 1e-21;
Matches 43; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47

RESULT 11
US-10-296-734-4
; Sequence 4, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VPR consensus polypeptide
US-10-296-734-4

Query Match          91.6%; Score 240; DB 15; Length 96;
Best Local Similarity 91.5%; Pred. No. 1e-21;
Matches 43; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47

RESULT 12
US-10-296-734-1475
; Sequence 1475, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1475
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-296-734-1475

Query Match          91.6%; Score 240; DB 15; Length 96;
Best Local Similarity 91.5%; Pred. No. 1e-21;
Matches 43; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
```

```
RESULT 13
US-10-190-435-258
; Sequence 258, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 258
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV008-17
US-10-190-435-258

Query Match          91.2%; Score 239; DB 14; Length 96;
Best Local Similarity 89.4%; Pred. No. 1.4e-21;
Matches 42; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47

RESULT 14
US-10-190-435-259
; Sequence 259, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 259
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV008-1
US-10-190-435-259

Query Match          91.2%; Score 239; DB 14; Length 96;
Best Local Similarity 89.4%; Pred. No. 1.4e-21;
Matches 42; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47

RESULT 15
US-10-190-435-273
; Sequence 273, Application US/10190435
```

```
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 273
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV012-4
US-10-190-435-273

Query Match          91.2%; Score 239; DB 14; Length 96;
Best Local Similarity 89.4%; Fred. No. 1.4e-21;
Matches 42; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 MEQAPDQGPQREPYNWTLLEELKSEAVRHPRIWLHNLGQHIY 47
        |||||
DB      1 MEQAPDQGPQREPYNWALEILEELKQEA VRHPRPWLHSLGQHIY 47
        |||||
```

Search completed: October 18, 2004, 18:52:22  
Job time : 85.1875 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:38:31 ; Search time 16.6458 Seconds  
(without alignments)  
271.671 Million cell updates/sec

Title: US-09-913-927D-2

Perfect score: 262

Sequence: 1 MEQAPDQGPQRPYNEWTLL.....SEAVRHFPRIWLHNLGQHIY 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	251	95.8	96	2 S54380	vpr protein - huma
2	247	94.3	95	2 T09383	vpr protein - huma
3	247	94.3	96	2 T09444	vpr protein - huma
4	242	92.4	96	2 T01670	vpr protein - huma
5	239	91.2	97	1 D44001	vpr protein - huma
6	215	82.1	96	1 ASLJSC	vpr protein - simi
7	154	58.8	97	2 S03067	gene R protein - h
8	148	56.5	101	1 ASLJR3	vpr protein - simi
9	147.5	56.3	122	1 ASLJRS	vpr protein - simi
10	145	55.3	89	2 S07991	vpr protein - simi
11	143	54.6	101	2 T11563	vpr protein - simi
12	134	51.1	104	2 S28083	vpr protein - simi
13	128	48.9	105	2 S53095	vpr protein - huma
14	125	47.7	101	2 S08439	vpr protein - huma
15	121	46.2	104	1 ASLJCY	vpr protein - huma
16	112.5	42.9	104	1 ASLJSY	vpr protein - huma
17	111	42.4	105	1 ASLJR2	vpr protein - huma
18	103	39.3	105	2 S12156	vpr protein - huma
19	94	35.9	105	1 ASLJGR	vpr protein - huma
20	87	33.2	140	2 S46351	vpx protein - simi
21	76.5	29.2	311	2 A10275	DNA replication te
22	67.5	25.8	119	1 ASLQX4	vpu protein - simi
23	64	24.4	508	1 P1WL	L1 protein - huma
24	63.5	24.2	154	2 S36993	transposase (clone
25	61	23.3	392	1 FOLJGA	gag polyprotein -
26	61	23.3	392	1 FOLJGB	gag polyprotein -
27	60.5	23.1	308	2 S29356	gag protein - bovi
28	60.5	23.1	308	2 B60672	blastula butanol-e
29	60.5	23.1	865	2 B64618	preprotein translo

blastula butanol-e  
hypothetical prote  
araC-like transcri  
probable chloropla  
transcription regu  
arac family transc  
agas protein - Esc  
hypothetical prote  
hypothetical prote  
orf-X protein - si  
vpu protein - simi  
vpu protein - simi  
gene X protein - h  
molybdopterin bios  
molybdopterin bios

#### ALIGNMENTS

##### RESULT 1

S54380

vpr protein - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004

C;Accession: S54380

R;Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A;Reference number: S54377

A;Accession: S54380

A;Status: preliminary

A;Molecule type: Genomic RNA

A;Residues: 1-96 <THE>

A;Cross-references: UNIPROT:P12519; EMBL:M22639; MID:g329377; PIDN:AAA45368.1; PID:g329377

C;Superfamily: AIDS vpr protein

Query Match 95.8%; Score 251; DB 2; Length 96;  
Best Local Similarity 95.7%; Pred. No. 1.5e-23;  
Matches 45; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPDQGPQRPYNEWTLLLEELKSEAVRHFPRIWLHNLGQHIY 47

Db 1 MEQAPDQGPQRPYNEWTLLLEELKSEAVRHFPRIWLHNLGQHIY 47

##### RESULT 2

T09383

vpr protein - human immunodeficiency virus type 1 (isolate cntrl 1)

C;Species: human immunodeficiency virus type 1, HIV-1

A;Variety: isolate cntrl 1

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: T09383

R;Michael, N.B.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Buech, M.P.; Birs

J. Virol. 69, 4228-4236, 1995

A;Title: Defective accessory genes in a human immunodeficiency virus type 1-infected long

A;Reference number: Z16654; MUID:95287475; PMID:7769682

A;Accession: T09383

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-95 <MTC>

A;Cross-references: UNIPROT:Q71925; EMBL:U24451; MID:g829440; PIDN:AAA79575.1; PID:g8294

C;Genetics:

A;Gene: vpr

C;Superfamily: AIDS vpr protein

C;Keywords: AIDS; immunodeficiency

Query Match 94.3%; Score 247; DB 2; Length 95;

Best Local Similarity 91.5%; Pred. No. 4.7e-23;

Matches 43; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEQAPDQGPQRPYNEWTLLLEELKSEAVRHFPRIWLHNLGQHIY 47

Db 1 MEQAPDQGPQRPYNEWTLLLEELKSEAVRHFPRIWLHNLGQHIY 47

```
Db 1 MERVPEQGPQREPYNWTLLELLEKSEAVRHFPRVWLHGLGQHIY 47
RESULT 3
T09444
vpr protein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09444
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09444
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-96 <PAN>
A:Cross-references: UNIPROT:Q75757; EMBL:U63632; NID:g1465777; PID:g1465784
C:Genetics:
A:Gene: vpr
C:Superfamily: AIDS vpr protein
Query Match 94.3%; Score 247; DB 2; Length 96;
Best Local Similarity 91.5%; Pred. No. 4.7e-23;
Matches 43; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQAPEDQGPQREPYNWTLLELLEKSEAVRHFPRVWLHGLGQHIY 47
Db 1 MEQAPEDQGPQREPYNWTLLELLEKSEAVRHFPRVWLHGLGQHIY 47
RESULT 4
T01670
vpr protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01670
R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A>Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol
A:Reference number: Z14389; MUID:86245056; PMID:2424612
A:Accession: T01670
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-96 <ALI>
A:Cross-references: UNIPROT:P05955; EMBL:K03456; NID:g60228; PIDN:CAA28014.1; PID:g60232
C:Superfamily: AIDS vpr protein
Query Match 92.4%; Score 242; DB 2; Length 96;
Best Local Similarity 91.5%; Pred. No. 1.9e-22;
Matches 43; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MEQAPEDQGPQREPYNWTLLELLEKSEAVRHFPRVWLHGLGQHIY 47
Db 1 MEQAPADQGPQREPYNWTLLELLEKSEAVRHFPRVWLHGLGQHIY 47
RESULT 5
D44001
vpr protein - human immunodeficiency virus type 1 (strain YU-2)
N:Alternate names: orf-R protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Accession: D44001
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A>Title: Complete nucleotide sequence, genome organization, and biological properties of
A:Reference number: A44001; MUID:93021387; PMID:1404605
A:Accession: D44001
A:Molecule type: DNA
A:Residues: 1-97 <LIY>
A:Cross-references: UNIPROT:P35967; GB:M93258
C:Genetics:
```

```
A:Gene: vpr
C:Superfamily: AIDS vpr protein
C:Keywords: AIDS; immunodeficiency
Query Match 91.2%; Score 239; DB 1; Length 97;
Best Local Similarity 91.5%; Pred. No. 4.5e-22;
Matches 43; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MEQAPEDQGPQREPYNWTLLELLEKSEAVRHFPRVWLHGLGQHIY 47
Db 1 MEQAPEDQGPQREPYNWTLLELLEKSEAVRHFPRVWLHGLGQHIY 47
RESULT 6
ASLJSC
vpr protein - simian immunodeficiency virus SIVcpz
N:Alternate names: orf-R protein
C:Species: simian immunodeficiency virus SIVcpz
A:Note: host Pan troglodytes (Chimpanzee)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S09986
R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A>Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:Reference number: S09983; MUID:90259077; PMID:2188136
A:Accession: S09986
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-96 <HUE>
A:Cross-references: UNIPROT:P17287; EMBL:X52154; NID:g58866; PIDN:CAA36403.1; PID:g58870
C:Genetics:
A:Gene: vpr
C:Superfamily: AIDS vpr protein
C:Keywords: AIDS; immunodeficiency
Query Match 82.1%; Score 215; DB 1; Length 96;
Best Local Similarity 83.0%; Pred. No. 3.7e-19;
Matches 39; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Qy 1 MEQAPEDQGPQREPYNWTLLELLEKSEAVRHFPRVWLHGLGQHIY 47
Db 1 MEQAPEDQGPQREPYNWTLLELLEKSEAVRHFPRVWLHGLGQFIY 47
RESULT 7
S03067
gene R protein - human T-cell lymphotropic virus type 4
C:Species: human T-cell lymphotropic virus type 4, HTLV-4
C>Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S03067
R:Hahn, B.H.; Kong, L.I.; Lee, S.W.; Kumar, P.; Taylor, M.E.; Arya, S.K.; Shaw, G.M.
Nature 300, 184-186, 1987
A>Title: Relation of HTLV-4 to simian and human immunodeficiency-associated viruses.
A:Reference number: S03065
A:Accession: S03067
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-97 <HAH>
A:Cross-references: UNIPROT:Q85605; EMBL:X06391; NID:g61580; PIDN:CAA29689.1; PID:g61582
C:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1987
C:Superfamily: AIDS vpr protein
Query Match 58.8%; Score 154; DB 2; Length 97;
Best Local Similarity 61.7%; Pred. No. 1e-11;
Matches 29; Conservative 10; Mismatches 6; Indels 2; Gaps 2;
Qy 2 EQAPEDQGPQREPYNWTLLELLEKSEAVRHF-PRVWLHGLGQHIY 47
Db 3 ERPPENEGPQREPWDEWVVEVLEELKEELKHPDRL-LTTLGNHIY 48
RESULT 8
ASLJK3
```

C;Genetics:  
A;Gene: vpr  
C;Superfamily: AIDS vpr protein

Query Match 55.3%; Score 145; DB 2; Length 89;  
Best Local Similarity 59.6%; Pred. No. 1.1e-10;  
Matches 28; Conservative 10; Mismatches 7; Indels 2; Gaps 2;

QY 2 EQAPEDGQGPPEYNWTLELLELKSEAVRHF-PRIVLHNLGHQHY 47  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
Db 3 ERPEDEAPQREPWDEWVVEVLKEELKBEALKHFDPRLL-LTALGNVIY 48

RESULT 11  
T11563  
vpr protein - simian immunodeficiency virus SIVsm (strain E543)  
C;Species: simian immunodeficiency virus SIVsm  
A;Variety: strain E543  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T11563  
J.R.Hirsch, V.M.; Adger-Johnson, D.; Cambell, B.; Goldstein, S.; Brown, C.; Elkins, W.R.; & N  
R.Virol. 71, 1608-1620, 1997  
A;Title: A molecularly cloned, pathogenic, neutralization-resistant simian immunodeficient  
A;Reference number: Z1285; MUID:97151152; PMID:8995688  
A;Accession: T11563  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-101 <HIR>  
A;Cross-references: UNIPROT:P89157; EMBL:U72748; NID:g1695908; PIDN:AAC56562.1; PID:g1695908  
C;Genetics:  
A;Gene: vpr  
C;Superfamily: AIDS vpr protein  
C;Keywords: AIDS; immunodeficiency

Query Match 54.6%; Score 143; DB 2; Length 101;  
Best Local Similarity 57.4%; Pred. No. 2.3e-10;  
Matches 27; Conservative 11; Mismatches 7; Indels 2; Gaps 2;

QY 2 EQAPEDGQGPPEYNWTLELLELKSEAVRHF-PRIVLHNLGHQHY 47  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
Db 3 ERPEDEAPQREPWDEWVVEVLKEELKBEALKHFDPRLL-LTALGNVIY 48

RESULT 12  
S28083  
vpr protein - simian immunodeficiency virus  
C;Species: simian immunodeficiency virus, SIV  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 24-Nov-1999  
C;Accession: S28083  
R.Tsujiimoto, H.; Hasegawa, A.; Makl, N.; Fukasawa, M.; Miura, T.; Speidel, S.; Cooper, R  
Nature 341, 539-541, 1999  
A;Title: Sequence of a novel simian immunodeficiency virus from a wild-caught African mar  
A;Reference number: S28080; MUID:90015168; PMID:2797181  
A;Accession: S28083  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-104 <TSU>  
A;Cross-references: GB:M27470; EMBL:X15781; NID:g334683; PIDN:AAB49571.1; PID:g334689  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1989  
C;Genetics:  
A;Gene: vpr  
C;Superfamily: AIDS vpr protein

Query Match 51.1%; Score 134; DB 2; Length 104;  
Best Local Similarity 52.3%; Pred. No. 3e-09;  
Matches 23; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 2 EQAPEDGQGPPEYNWTLELLELKSEAVRHF-PRIVLHNLGHQ 45  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
Db 7 EQVSEDGQPPREPNQWLADTMEEKBEARKHFPPLIILNAVSEY 50

RESULT 13

Search completed: October 18, 2004, 18:48:20  
Job time : 17.6458 secg

vpr protein - human immunodeficiency virus type 2 (isolate CAM2/Guinea-Bissau)  
N;Alternate names: orf-R protein  
C;Species: human immunodeficiency virus type 2, HIV-2  
A;Note: host Homo sapiens (man)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C;Accession: E38475, JQ0977  
R;Tristram, M.; Hill, F.; Karpas, A.  
J. Gen. Virol. 72, 721-724, 1991  
A;Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus type  
A;Reference number: A38475; MUID:91170959; PMID:2005437  
A;Accession: E38475  
A;Molecule type: DNA  
A;Residues: 1-104 <TRI>  
A;Cross-references: UNIPROT:P24111; GB:D00835; NID:G3153166; PIDN:BA00713.1; PID:g22147  
C;Genetics:  
A;Gene: vpr  
C;Superfamily: AIDS vpr protein



Q73733; 01-NOV-1996 (TREMBlrel. 01, Created)

DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)
DE	Vpr protein.	
GN	Name=vpr;	
OS	Human immunodeficiency virus 1.	
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.	
OX	NCBI_TaxID=11676;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=86259728; PubMed=3014529;	
RA	Willey R.L., Rutledge R.A., Dias S., Folke T., Theodore T.,	
RA	Buckler C.E., Martin M.A.;	
RT	"Identification of conserved and divergent domains within the envelope	
RT	gene of the acquired immunodeficiency syndrome retrovirus.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 83:5038-5042(1986).	
DR	EMBL; M38431; AAB04039.1; -;	
DR	HSSP; P12520; 1DSJ.	
DR	InterPro; IPR000012; RetroV_Vpr/X.	
DR	Pfam; PF00522; VPR; 1.	
DR	PRINTS; PR00444; HIVPRVPX.	
KW	AIDS.	
SQ	SEQUENCE 96 AA; 11377 MW; 58BC535543D87250 CRC64;	
Query Match 100.0%; Score 262; DB 2; Length 96;		
Best Local Similarity 100.0%; Pred. No. 1.2e-24;		
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Oy	1	MEQAPDQGQREPYNEWTLLELLELSEAVRHFPRIWLNLGHQIY 47
Db	1	MEQAPDQGQREPYNEWTLLELLELSEAVRHFPRIWLNLGHQIY 47
RESULT 3		
Q99DD7	ID	Q99DD7 PRELIMINARY; PRT; 96 AA.
AC	Q99DD7;	
DT	01-JUN-2001	(TrEMBLrel. 17, Created)
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)
DE	Vpr protein.	
GN	Name=vpr;	
OS	Human immunodeficiency virus 1.	
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.	
OX	NCBI_TaxID=11676;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=21268767; PubMed=11375060;	
RA	Halani N., Wang B., Ge Y.C., Ghardure H., Hira S., Saksena N.K.;	
RT	"Changing epidemiology of HIV type 1 infections in India: evidence of	
RT	subtype B introduction in Bombay from a common source.";	
RL	AIDS Res. Hum. Retroviruses 17:637-642(2001).	
DR	EMBL; AF16101; AAK11289.1; -;	
DR	HSSP; P12520; 1DSJ.	
DR	InterPro; IPR000012; RetroV_Vpr/X.	
DR	Pfam; PF00522; VPR; 1.	
KW	AIDS.	
SQ	SEQUENCE 96 AA; 11372 MW; 58BC53558EB286D4F CRC64;	
Query Match 99.6%; Score 261; DB 2; Length 96;		
Best Local Similarity 97.9%; Pred. No. 1.7e-24;		
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Oy	1	MEQAPDQGQREPYNEWTLLELLELSEAVRHFPRIWLNLGHQIY 47
Db	1	MEQAPDQGQREPYNEWTLLELLELSEAVRHFPRIWLNLGHQIY 47
RESULT 4		
Q99DD8	ID	Q99DD8 PRELIMINARY; PRT; 96 AA.
AC	Q99DD8;	
DT	01-JUN-2001	(TrEMBLrel. 17, Created)
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)

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DE Vpr protein (Fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R.; Chappey C.; Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042912; AAC41079.1; -.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 11416 MW; DB95484EC487E220 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHFPRIWLHNLGHQIY 47
Db 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHFPRIWLHNLGHQIY 47

RESULT 7
O89603 PRELIMINARY; PRT; 96 AA.
AC O89603;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein (Fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R.; Chappey C.; Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042913; AAC41080.1; -.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHFPRIWLHNLGHQIY 47
Db 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHFPRIWLHNLGHQIY 47

RESULT 8
O89604 PRELIMINARY; PRT; 96 AA.
AC O89604;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vpr protein (Fragment).
```

```
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R.; Chappey C.; Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042915; AAC41081.1; -.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 11432 MW; DB954C0F2C808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHFPRIWLHNLGHQIY 47
Db 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHFPRIWLHNLGHQIY 47

RESULT 9
O89606 PRELIMINARY; PRT; 96 AA.
AC O89606;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein (Fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R.; Chappey C.; Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042917; AAC41083.1; -.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHFPRIWLHNLGHQIY 47
Db 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHFPRIWLHNLGHQIY 47

RESULT 10
O89608 PRELIMINARY; PRT; 96 AA.
AC O89608;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vpr protein (Fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
```

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OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R.; Chappey C.; Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042921; AAC41085.1; -.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLELSEAVRHFPRWLHNLGQHIY 47
Db 1 MEQAPEDQGPQREPYNEWTLLELSEAVRHFPRWLHNLGQHIY 47

RESULT 11
O89609
ID O89609 PRELIMINARY; PRT; 96 AA.
AC O89609;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein (fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R.; Chappey C.; Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042920; AAC41086.1; -.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLELSEAVRHFPRWLHNLGQHIY 47
Db 1 MEQAPEDQGPQREPYNEWTLLELSEAVRHFPRWLHNLGQHIY 47

RESULT 12
O89610
ID O89610 PRELIMINARY; PRT; 96 AA.
AC O89610;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein (fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

```

```

OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R.; Chappey C.; Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042921; AAC41087.1; -.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLELSEAVRHFPRWLHNLGQHIY 47
Db 1 MEQAPEDQGPQREPYNEWTLLELSEAVRHFPRWLHNLGQHIY 47

RESULT 13
O89611
ID O89611 PRELIMINARY; PRT; 96 AA.
AC O89611;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein (fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R.; Chappey C.; Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042922; AAC41088.1; -.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLELSEAVRHFPRWLHNLGQHIY 47
Db 1 MEQAPEDQGPQREPYNEWTLLELSEAVRHFPRWLHNLGQHIY 47

RESULT 14
O89612
ID O89612 PRELIMINARY; PRT; 96 AA.
AC O89612;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vpr protein (fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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RN SEQUENCE FROM N.A.
RP MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R., Chappey C., Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042923; AAC41089.1; -.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match      98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGQFPQRYNEWTLLELLEKSEAVRHPRIWLHNLGQHIY 47
Db 1 MEQAPEDQGQFPQRYNEWTLLELLEKSEAVRHPRIWLHNLGQHIY 47

RESULT 15
O89613
AC O89613; PRELIMINARY; PRT; 96 AA.
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein (Fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_taxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R., Chappey C., Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042924; AAC41090.1; -.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match      98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGQFPQRYNEWTLLELLEKSEAVRHPRIWLHNLGQHIY 47
Db 1 MEQAPEDQGQFPQRYNEWTLLELLEKSEAVRHPRIWLHNLGQHIY 47
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Search completed: October 18, 2004, 18:47:36  
Job time : 59.75 secs



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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:31:42 ; Search time 64.3125 Seconds  
(without alignments)  
273.318 Million cell updates/sec

Title: US-09-913-927D-3

Perfect score: 254

Sequence: 1 ETYGDWTWAGVEAIRILQQL.....RHSRIGVTRQRRNRCASRS 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254	100.0	49	3 AAB10687	Aab10687 HIV-1 reg
2	254	100.0	96	2 AAR48963	Aar48963 HIV VPr.
3	254	100.0	96	2 AAW53040	Aaw53040 HIV-1 pol
4	254	100.0	96	3 AAB10049	Aab10049 HIV-1 vpr
5	254	100.0	96	3 AAB10685	Aab10685 HIV-1 reg
6	254	100.0	96	5 AAE16129	Aae16129 Human imm
7	254	100.0	96	5 ABP56175	Abp56175 HIV-1 vir
8	254	100.0	96	5 AAU80187	Aau80187 HIV-1 Vpr
9	254	100.0	96	7 ADD01277	Adg01277 HIV-1 Vpr
10	254	100.0	96	8 ADF46812	Adf46812 HIV-1 Vpr
11	254	100.0	96	8 ABM79669	Abm79669 HIV-1 Vpr
12	253	99.6	96	8 ADP20070	Adp20070 Human imm
13	250	98.4	95	8 ADP81477	Adp81477 HIV-1 vpr
14	250	98.4	96	2 AAR94544	Aar94544 Native Vp
15	250	98.4	96	3 AAY53247	Aay53247 HIV-1 LAI
16	249	98.0	96	6 ABR55491	Abr55491 Amino aci
17	249	98.0	96	8 ADP20078	Adp20078 Human imm
18	244	96.1	96	3 AAB69306	Aab69306 HIV-1 non
19	243	95.7	3032	8 ADP81468	Adp81468 Lymphaden
20	243	95.7	3033	7 ADA49379	Ada49379 Lymphaden
21	242	95.3	96	2 AAR10175	Aar10175 Rap (R) p
22	241	94.9	96	2 AAR12258	Aar12258 HIV-1 str
23	238	93.7	96	3 AAB69304	Aab69304 HIV-1 non
24	238	93.7	96	3 AAB69308	Aab69308 HIV-1 non
25	236	92.9	96	1 AAP81856	Aap81856 Sequence

#### ALIGNMENTS

##### RESULT 1

AAB10687

ID AAB10687 standard; peptide; 49 AA.

AC AAB10687;

XX 19-JAN-2001 (first entry)

DE HIV-1 regulatory virus protein R peptide sVpr48-96.

XX Regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity;  
KW structural analysis; cell cycle arrest.

XX Synthetic.

OS Human immunodeficiency virus 1.

PN WO200049038-A2.

XX 24-AUG-2000.

PF 19-FEB-2000; 2000WO-DE000525.

XX 19-FEB-1999; 99DE-01008752.

PR 19-FEB-1999; 99DE-01008766.

XX (SCHU/) SCHUBERT U.

PA (HENK/) HENKLEIN P.

XX (WRAY/) WRAY V.

XX Schubert U, Henklein P, Wray V;

DR WPI; 2000-565367/52.

XX New synthetic peptides from the Vpr protein of human immune deficiency

PT virus, useful e.g. for therapy and diagnosis, have good solubility in

water.

XX Claim 3.3; Page 5; 35pp; German.

PS This invention describes novel synthetic peptides (I) derived from the

XX regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-

CC 1) which have antiviral activity and can be used for gene therapy. (I) is

CC used for therapeutic and/or diagnostic purposes, especially in biological

CC assays, for development of serological tests or enzyme-linked

CC immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in

CC blood), to raise specific antibodies and antisera (especially those

CC reactive with specific epitopes), and as antiviral agents. (I) can also

CC be used in screening for potential Vpr antagonists (i.e. compounds that

CC

CC modulate interaction of Vpr with cellular factors, transcription-  
 CC activating properties of Vpr, transport of Vpr and its incorporation into  
 CC viral particles, Vpr-induced cell cycle arrest, and cytotoxic and ion-  
 CC channel activities of Vpr. (I) is used to establish cell or animal  
 CC models for studying pathogenicity of Vpr, for structural analysis of Vpr  
 CC and its domains, for in vitro assembly of new vectors for gene therapy,  
 CC in vitro or in vivo, for complementing the function of Vpr-defect mutants  
 CC in cell cultures, and to reduce flexibility of Vpr induced by the N-  
 CC terminal domain. Synthetic (I), are soluble in water and can be  
 CC aggregated as highly concentrated solutions (mmolar) without protein  
 CC resonance, so are well suited to analysis by nuclear magnetic  
 CC structure, X-ray or circular dichroism techniques. (I) adopt a folded  
 CC can be produced, at high purity, on the milligram scale. This sequence  
 CC represents the synthetic HIV-1 derived Vpr peptide svpr48-96 which is  
 CC used in the method of the invention  
 CC  
 XX  
 SQ Sequence 49 AA;  
 Query Match 100.0%; Score 254; DB 3; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 7e-30; Indels 0; Gaps 0;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ETYGDWTAGVEAIRIILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49  
 |||||  
 DB 1 ETYGDWTAGVEAIRIILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49  
 |||||  
 RESULT 2  
 AAR48963  
 ID AAR48963 standard; protein; 96 AA.  
 XX  
 AC AAR48963;  
 DT 25-MAR-2003 (revised)  
 DT 12-SEP-1994 (first entry)  
 XX  
 DE HIV VPR.  
 KW HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;  
 KW naturally occurring virus; NOV; translation; replication; infectivity;  
 KW hepatitis B; HIV-2; SIV; flip-over PCR.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9403596-A1.  
 XX  
 PD 17-FEB-1994.  
 XX  
 PF 30-JUL-1993; 93WO-US007179.  
 XX  
 PR 30-JUL-1992; 92US-00921104.  
 XX  
 PA (UYHA-) UNIV HAWAII.  
 XX  
 PI Hu W, Wang J;  
 XX  
 XX WPI; 1994-065685/08.  
 DR N-PSDB; AAQ48962.  
 XX  
 PT New antisense viruses and anti-sense-ribosome viruses - used for treating  
 PT or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.  
 XX  
 PS Disclosure; Page 111; 167pp; English.  
 XX  
 CC This sequence represents the "perfect" VPR protein encoded by the PCR  
 CC fragment of pX-CS which encoded the truncated gag gene and the "perfect"  
 CC vpr gene. The cDNA fragment encoding this protein was used to produce the  
 CC antisense virus of the invention. Antisense or truncated RNAs expressed  
 CC by these viruses bind to the mRNAs expressed by the naturally occurring  
 CC viruses (NOVs) and prevent the mRNAs from being translated into proteins,  
 CC thereby preventing the NOV from replicating. The antisense viruses  
 CC maintain the infectivity of the NOVs, allowing antisense RNAs to reach

CC the mRNAs of the natural viruses. Antisense viruses such as these may be  
 CC used for treating or preventing a viral infection, particularly HIV-1,  
 CC HIV-2 or SIV infection or hepatitis B infection. (Updated on 25-MAR-2003  
 CC to correct PN field.)  
 XX  
 SQ Sequence 96 AA;  
 Query Match 100.0%; Score 254; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-29;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ETYGDWTAGVEAIRIILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49  
 |||||  
 DB 48 ETYGDWTAGVEAIRIILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96  
 |||||  
 RESULT 3  
 AAW53040  
 ID AAW53040 standard; peptide; 96 AA.  
 XX  
 AC AAW53040;  
 DT 17-OCT-2003 (revised)  
 DT 17-JUL-1998 (first entry)  
 XX  
 DE HIV-1 polypeptide.  
 XX  
 KW Recombinant plant virus; HIV-1; protein production; immunisation;  
 KW fusion capsid protein; alfalfa mosaic virus; iliarvirus; pathogen;  
 KW rhabdovirus.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 XX WO9808375-A1.  
 XX  
 PD 05-MAR-1998.  
 XX  
 PF 28-AUG-1997; 97WO-US015200.  
 XX  
 PR 28-AUG-1996; 96US-00704856.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Koprowski H, Hooper DC, Yusibov V, Modelska A;  
 XX  
 DR WPI; 1998-179070/16.  
 XX  
 PT Production of poly:peptide(s), particularly for use in vaccines - by  
 PT expression as fusion proteins with plant virus capsid protein in plant  
 PT cells infected with virus.  
 XX  
 PS Disclosure; Page 4; 63pp; English.  
 XX  
 CC This sequence is a HIV-1 polypeptide that can be used in a recombinant  
 CC plant virus used in the process of the invention. The process is for  
 CC administering a polypeptide to an animal comprising: (a) infecting a  
 CC plant cell with recombinant plant virus nucleic acid that will be  
 CC processed in a plant cell to produce a fusion capsid protein (FCP), the  
 CC FCP comprises a plant virus capsid protein (PVCp) and a polypeptide that  
 CC is not a PVCp, the PVCp being an alfalfa mosaic virus (AMV) capsid  
 CC protein (CP) or iliarvirus CP thereby creating a infected cell; (b)  
 CC culturing the infected cell, or a derivative cell derived from the  
 CC infected cell, under conditions where the infected cell or derivative  
 CC cell makes the FCP; and (c) administering the FCP or a portion to an  
 CC animal. The recombinant plant virus can also be used for production of  
 CC polypeptides. The method is used particularly for the production of  
 CC polypeptides which can be used for immunisation against pathogens such as  
 CC rhabdovirus or HIV. (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 96 AA;  
 Query Match 100.0%; Score 254; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-29;



Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRARNGASRS 49  
 |||||  
 Db 48 ETYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 4  
 AAB10049  
 ID AAB10049 standard; protein; 96 AA.  
 XX  
 AC AAB10049;  
 XX  
 XX 12-SEP-2003 (revised)  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE HIV-1 vpr protein.  
 XX  
 XX Glycoprotein; gag; pol; GP-1; GP-2; anti-HIV; cytostatic; gene therapy;  
 KW treatment; infectious disease; HIV; AIDS; neoplasm; carcinoma; melanoma;  
 KW vpr protein.  
 XX  
 XX Human immunodeficiency virus 1.  
 OS  
 XX  
 PN EP1006196-A2.  
 XX  
 XX 07-JUN-2000.  
 XX  
 XX 25-NOV-1999; 99EP-00250415.  
 PF  
 XX 26-NOV-1998; 98DE-01056463.  
 PR  
 XX (PETT-) PETTE INST HEINRICH.  
 PA  
 XX Von Laer MD;  
 PI  
 XX WPI; 2000-378268/33.  
 DR  
 XX N-PSDB; AAA40298, AAB10053, AAB10054.  
 DR  
 XX New retroviral packing cell useful as pharmaceutical carrier in gene  
 PT therapy for treatment of HIV and neoplasms, comprises retroviral genes  
 PT and glycoproteins.  
 PT  
 XX Disclosure; Page 44; 69pp; German.  
 PS  
 XX This invention describes a novel retroviral packing cell (I), comprising  
 CC the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV  
 CC coding gene gp, or a part of these. The products of the invention have  
 CC anti-HIV and cytostatic activity and can be used for gene therapy. (I) is  
 CC useful for in vitro infection of cells, especially hematopoietic stem  
 CC cells, for expression of transgenes in cells and as a pharmaceutical  
 CC carrier for gene therapy. (I) is therefore useful in the treatment of  
 CC infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and  
 CC other diseases. This sequence represents the Human immunodeficiency virus  
 CC (HIV-1) vpr protein described in the method of the invention. (Updated on  
 CC 12-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 96 AA;

Query Match 100.0%; Score 254; DB 3; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-29;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRARNGASRS 49  
 |||||  
 Db 48 ETYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 5  
 AAB10685  
 ID AAB10685 standard; peptide; 96 AA.  
 XX  
 AC AAB10685;

XX 19-JAN-2001 (first entry)  
 DT  
 XX HIV-1 regulatory virus protein R peptide svpr1-96.  
 DE  
 XX Regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity;  
 KW structural analysis; cell cycle arrest.  
 KW  
 XX Synthetic.  
 OS  
 XX Human immunodeficiency virus 1.  
 PN WO200049038-A2.  
 XX  
 XX 24-AUG-2000.  
 PD  
 XX 19-FEB-2000; 2000WO-DE0000525.  
 PF  
 XX 19-FEB-1999; 99DE-01008752.  
 PR  
 XX 19-FEB-1999; 99DE-01008766.  
 PR  
 XX (SCHU/) SCHUBERT U.  
 PA (HENK/) HENKLEIN P.  
 PA (WRAY/) WRAY V.  
 XX  
 XX Schubert U, Henklein P, Wray V;  
 PI WPI; 2000-565367/52.  
 DR  
 XX New synthetic peptides from the Vpr protein of human immune deficiency  
 PT virus, useful e.g. for therapy and diagnosis, have good solubility in  
 PT water.  
 PT  
 XX Claim 3.1; Page 5; 35pp; German.  
 PS  
 XX This invention describes novel synthetic peptides (I) derived from the  
 CC regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-  
 CC 1) which have antiviral activity and can be used for gene therapy. (I) is  
 CC used for therapeutic and/or diagnostic purposes, especially in biological  
 CC assays, for development of serological tests or enzyme-linked  
 CC immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in  
 CC blood), to raise specific antibodies and antisera (especially those  
 CC reactive with specific epitopes), and as antiviral agents. (I) can also  
 CC be used in screening for potential Vpr antagonists (i.e. compounds that  
 CC modulate interaction of Vpr with cellular factors, transcription-  
 CC activating properties of Vpr, transport of Vpr and its incorporation into  
 CC viral particles, Vpr-induced cell cycle arrest, and cytotoxic and ion-  
 CC channel activities of Vpr). (I) is used to establish cell or animal  
 CC models for studying pathogenicity of Vpr, for structural analysis of Vpr  
 CC and its domains, for in vitro assembly of new vectors for gene therapy,  
 CC in vitro or in vivo, for complementing the function of Vpr-defect mutants  
 CC in cell cultures, and to reduce flexibility of Vpr induced by the N-  
 CC terminal domain. Synthetic (I), are soluble in water and can be  
 CC formulated as highly concentrated solutions (mmolar) without protein  
 CC aggregation, so are well suited to analysis by nuclear magnetic  
 CC resonance, x-ray or circular dichroism techniques. (I) adopt a folded  
 CC structure, have biological activity comparable to that of viral Vpr, and  
 CC can be produced, at high purity, on the milligram scale. This sequence  
 CC represents the synthetic HIV-1 derived Vpr peptide svpr1-96 which is used  
 CC in the method of the invention  
 XX  
 SQ Sequence 96 AA;

Query Match 100.0%; Score 254; DB 3; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-29;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRARNGASRS 49  
 |||||  
 Db 48 ETYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 6  
 AAB16129

AAE16129 standard; protein; 96 AA.  
AAE16129;  
29-AUG-2003 (revised)  
26-MAR-2002 (first entry)  
Human immunodeficiency virus type 1 (HIV-1) sVpr protein.  
Human immunodeficiency virus type 1; HIV-1; auxiliary protein; cancer;  
Vpr protein; regulatory protein; pathogen; cell proliferation; therapy;  
dysregulated cell growth; hyperproliferative cell disorder; malignancy;  
radiation therapy; psoriasis; transgene expression; immune response;  
cytostatic; apoptotic.  
Human immunodeficiency virus 1.  
Key Location/Qualifiers  
Region 17..29  
/label= Alpha\_1\_helix  
Region 36..47  
/label= Alpha\_2\_helix  
Region 53..78  
/label= Alpha\_3\_helix  
WO200190159-A2.  
29-NOV-2001.  
23-MAY-2001; 2001WO-US016943.  
23-MAY-2000; 2000US-0206610P.  
09-FEB-2001; 2001US-0267827P.  
20-APR-2001; 2001US-00839329.  
(GLAD-) GLADSTONE INST J DAVID.  
(SCHU/) SCHUBERT U.  
(HENK/) HENKLEIN P.  
Schubert U, Henklein P, Sherman MP, Greene WC, De Noronha CMC;  
WPI; 2002-083087/11.  
Delivering molecule into cell for inhibiting cell proliferation and  
killing target cell, comprises contacting cell with Vpr polypeptide,  
regulatory protein encoded by HIV type 1, alone or conjugated to  
molecule.  
Example 1; Fig 1A; 72pp; English.  
The present invention relates to compositions comprising Vpr polypeptides  
conjugated to a therapeutic molecule. Vpr polypeptides are regulatory or  
auxiliary proteins encoded by a lentivirus, human immunodeficiency virus  
type 1 (HIV-1). The invention also relates to a method for delivering a  
molecule into a cell which comprises contacting the cell with a conjugate  
comprising a Vpr polypeptide conjugated to the molecule. The method is  
useful for delivering a polypeptide, polynucleotide (DNA or RNA) or a  
toxin into a cell, preferably a cancer cell, or a cell infected with a  
pathogen such as lentivirus, HIV or retrovirus, bacterium or a parasite.  
Compositions comprising Vpr polypeptide conjugated to a toxin is useful  
for killing a cancer cell or a cell infected with a pathogen where the  
toxin is further conjugated to a regulatory molecule and the contact with  
the target cell exerts an effect on the regulatory molecule that results  
in activation of the toxin. The method is useful for inhibiting cell  
proliferation and treating a disorder associated with dysregulated cell  
growth in a subject. Vpr polypeptides when administered alone are useful  
for increasing sensitivity to radiation therapy in a subject undergoing  
radiation therapy. They can also be used to treat hyperproliferative cell  
disorders such as malignancies, psoriasis and other disorders associated  
with dysregulated cell growth. Vpr polypeptides conjugated to a  
regulatory moiety is useful for modulating the expression of a transgene  
in a cell. Vpr polypeptides alone or conjugated to an antigen is useful  
for increasing an immune response. The present sequence is synthetic Vpr

(sVpr) protein from HIV-1. (Updated on 29-AUG-2003 to standardise OS  
field)  
XX Sequence 96 AA;  
Query Match 100.0%; Score 254; DB 5; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.5e-29;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Ov 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 49  
|||||  
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 96  
|||||  
RESULT 7  
ABP56175  
ID ABP56175 standard; peptide; 96 AA.  
XX  
AC ABP56175;  
XX  
DT 29-AUG-2003 (revised)  
DT 28-MAR-2003 (first entry)  
XX  
DE HIV-1 viral protein R (Vpr) amino acid sequence.  
XX  
KW Mitochondrial membrane permeabilisation; mitochondrion; PTPC;  
KW permeability transition pore complex; virucide; neuroprotective;  
KW vasotrophic; cytostatic; infection; cell death regulation; apoptosis;  
KW mitochondrial permeability transition pore complex modulator; cancer;  
KW apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200261105-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 01-FEB-2002; 2002WO-EP001633.  
XX  
PR 02-FEB-2001; 2001US-0265594P.  
XX  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CENT NAT RECH SCI.  
XX  
PI Edelman L, Jacotot E, Briand J;  
XX  
DR WPI; 2002-619260/66.  
XX  
PT New chimeric bifunctional molecules that target specific cells and  
regulate the apoptosis function of the permeability transition pore  
complex of the mitochondria, useful for treating or preventing e.g.  
cancer or ischemia.  
XX  
PS Disclosure; Page 13; 76pp; English.  
XX  
CC The present invention describes a chimeric bifunctional molecule (I)  
comprising at least a first functional molecule covalently linked to a  
second functional molecule, which is able to modulate the activity of the  
permeability transition pore complex (PTPC) of the mitochondria. (I) has  
the function of specifically targeting and entering a tissue cell  
population. The second functional molecule has the function of  
specifically targeting, and inducing or preventing the death of the cells  
by apoptosis by regulating the opening or the closing of the PTPC of the  
mitochondria or its fragment. (I) has virucide, neuroprotective,  
vasotrophic and cytostatic activities, and can be used as a mitochondrial  
permeability transition pore complex (PTPC) modulator. (I) is useful for  
treating or preventing a pathological infection or disease. (I) is also  
useful for regulating cell death regulatory molecules, specifically the  
apoptogenic function of the PTPC, for treating e.g. cancer, ischaemia,  
neurodegenerative diseases, fulminant hepatitis or viral infections. The  
present sequence represents the HIV-1 viral protein R (Vpr) amino acid  
sequence, which is given in the exemplification of the present invention.  
(Updated on 29-AUG-2003 to standardise OS field)

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XX SQ Sequence 96 AA;
Query Match 100.0%; Score 254; DB 5; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
Dy 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 8
ID AAU80187 standard; protein; 96 AA.
AC AAU80187;
XX 29-AUG-2003 (revised)
DT 15-JUL-2002 (first entry)
XX HIV-1 Vpr protein.
XX HIV-1; acquired immunodeficiency syndrome; AIDS; Vpr.
XX Human immunodeficiency virus 1.
XX Key Location/Qualifiers
XX Misc-difference 45 /note= "Encoded by CAT"
XX JF2002085099-A.
XX 26-MAR-2002.
XX 14-SEP-2000; 2000JP-00280851.
XX 14-SEP-2000; 2000JP-00280851.
XX (KOKU-) KOKURITSU YOB0 EISEI KENKYUSHO.
XX (ORIY) ORIENTAL YEAST CO LTD.
XX WPI; 2002-378279/41.
XX N-PSDB; ABK50386.
XX Detection of immunodeficiency virus by detecting the presence of Vpr protein.
XX Disclosure; Page 8; 17pp; Japanese.
XX The invention relates to a method for detecting immunodeficiency virus in a sample in which the presence of Vpr (not defined) protein in the sample is detected. Also included are a kit for use in the above detecting a method containing a cell and a pigment, and a method for screening a compound promoting or inhibiting the intake of a substance having a molecular weight (M.W.) of 300 to 3000 in which the promotion or the inhibition of intake of the substance by the presence of a test compound is used as the index in the intake of the substance to the cell by a treatment using a sample containing Vpr protein. The method is used for detecting immunodeficiency virus (e.g. Human immunodeficiency virus-1, the causative agent of acquired immunodeficiency virus syndrome, AIDS) in a sample. The present sequence represents HIV-1 Vpr. (Updated on 29-AUG-2003 to standardise OS field)
XX Sequence 96 AA;
Query Match 100.0%; Score 254; DB 5; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
Dy 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

us-09-913-927d-3.rag
RESULT 9
ADD01277
ID ADD01277 standard; protein; 96 AA.
XX ADD01277;
XX 01-JAN-2004 (first entry)
XX HIV-1 Vpr CyPA protein binding motif.
XX lentivirus protein R; Vpr; inhibitor; cellular chaperone; folding; stability; cyclophilin A; CyPA; cell-cycle arrest; apoptosis; glucocorticoid receptor coactivation; anti-HIV; neurotropic; nephrotropic; antileptic; antiretroviral; AIDS; infection; HIV-induced dementia; lipodystrophy syndrome; lipid metabolism; HIV-associated nephropathy.
XX Human immunodeficiency virus 1.
XX WO2003038032-A2.
XX 08-MAY-2003.
XX 25-OCT-2002; 2002WO-DE004052.
XX 25-OCT-2001; 2001DE-01053902.
XX (MEDI-) MEDICIS VENTURES MANAGEMENT GMBH.
XX Will H, Tessmer U, Bruns K;
XX WPI; 2003-430506/40.
XX Agent for inhibiting lentivirus Vpr protein, useful for treatment and prevention of infection by human immune deficiency virus, is inhibitor of chaperone enzyme.
XX Disclosure; Fig 4; 41pp; German.
XX This invention describes a novel agent (A), for inhibiting the primate lentivirus protein R (Vpr) of HIV-1 or -2, or simian immune deficiency virus, comprising an inhibitor (I) of cellular chaperones (II) that are essential for proper folding, stability and, thus, biological function of Vpr. The inhibitor is useful for inhibiting interaction of Vpr with cyclophilins include cyclosporin A, FK506, rapamycin and the non-immunosuppressive compounds SDZ NIM811 and/or sangliferin A. Vpr first binds to cyclophilin A (CyPA) to regulate the trans conformation of proline peptidyl bonds in the N-terminus of Vpr. The inhibitor prevents cis-trans rearrangement, specifically of pro residues at positions 5, 10, 14 and 35 of Vpr. The inhibitor may also act by a process in which CyPA co-translationally regulates expression, folding and stability of Vpr and this stabilizing process is active in cells transfected with the specified viruses, with DNA that encodes Vpr, or with recombinant Vpr-encoding retro, adeno, vaccinia or baculo viruses. All essential functions of Vpr (induction of cell-cycle arrest, apoptosis, increased viral production and co-activation of glucocorticoid receptors) are inhibited. The products of the invention have anti-HIV, neurotropic, nephrotropic and antileptic activity. The inhibitor may be used in combination with other antiretroviral agents; blockers of reverse transcription and/or protease; genetically based antiretroviral therapies, intracellular immunization and administration of anti-HIV gene in stem cells and/or peripheral CD4+ lymphocytes, especially in advanced stages of disease. The agent of the invention is used to prevent and treat lentiviral infections, specifically AIDS or HIV infections (including where asymptomatic), also HIV-induced dementia (by inhibiting infection of neurons, glial cells and endothelial cells in cerebral capillaries), HIV-associated lipodystrophy syndrome or other disorders of lipid metabolism and HIV-associated nephropathy, also to prevent systemic infection immediately after exposure to HIV, e.g. needle pricks with HIV-contaminated blood. This sequence represents the CyPA binding fragment at the N-terminal of the HIV-1(NL4-3) Vpr protein.

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SQ Sequence 96 AA;
Query Match      100.0%; Score 254; DB 7; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
    |||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 10
ADF46812
ID ADF46812 standard; protein; 96 AA.
XX
AC ADF46812;
XX
DT 12-FEB-2004 (first entry)
XX
DE HIV-1 Vpr protein.
XX
KW virus protein R; Vpr; functional analysis.
XX
OS Human immunodeficiency virus 1.
XX
PN JP2003259881-A.
XX
PD 16-SEP-2003.
XX
PF 12-MAR-2002; 2002JP-00066938.
XX
PR 12-MAR-2002; 2002JP-00066938.
XX
PA (ORIY) ORIENTAL YEAST CO LTD.
PA (NAKA) NAKAMURA T.
XX
DR WPI; 2004-026590/03.
DR N-PSDB; ADF46813.
XX
PT Producing recombinant virus protein R (Vpr), useful in promoting
PT immunodeficiency virus reproduction, involves transforming a host cell
PT with an expression vector for the protein.
XX
PS Claim 1; SEQ ID NO 1; 14pp; Japanese.
XX
CC The invention relates to a method of producing a recombinant HIV-1 virus
CC protein R (Vpr) protein or a protein having one or more substitutions,
CC additions or alterations and having biological activity, by transforming
CC a host Escherichia coli cell with an expression vector containing the
CC gene encoding Vpr, and culturing the transformed cell. The method is
CC useful for producing recombinant Vpr protein. The protein is useful for
CC promoting the reproduction of immunodeficiency virus in cell, tissue or
CC organ derived from an organism. The protein is useful for functional
CC analysis of the Vpr protein. This sequence represents the HIV-1 Vpr
CC protein.
XX
SQ Sequence 96 AA;

Query Match      100.0%; Score 254; DB 8; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
    |||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 11
ABM79669
ID ABM79669 standard; protein; 96 AA.
XX
AC ABM79669;
XX

22-APR-2004 (first entry)
HIV-1 Vpr protein.
HIV; Vpr; modulator; anti-HIV; virucide.
Human immunodeficiency virus type 1.
WO2003076621-A2.
18-SEP-2003.
07-MAR-2003; 2003WO-CA000325.
08-MAR-2002; 2002US-0362384P.
(UYMO-) UNIV MONTREAL.
Cohen EA, Yao X, Belhumeur P, Lemay J;
WPI; 2004-042337/04.
New polypeptides that bind to viral Vpr protein, useful for treatment,
prevention, diagnosis and prognosis of immune deficiency virus infection.
Example 20; Page 33-34; 143pp; English.
The present invention relates to peptide which are capable of binding to
the HIV protein Vpr and/or modulates Vpr-related activity. Such peptides
are used for prevention, treatment, diagnosis and prognosis of Vpr-
related diseases, particularly lentiviral infection (specifically HIV-1
or -2, or simian immune deficiency virus), for modulating, particularly
inhibiting, Vpr-related activities and for detecting Vpr in a sample.
Nucleic acids encoding such peptides and cells that contain this nucleic
acid can also be used therapeutically. The present sequence is a protein
of relevance to the invention
SQ Sequence 96 AA;

Query Match      100.0%; Score 254; DB 8; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
    |||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 12
ADP20070
ID ADP20070 standard; protein; 96 AA.
XX
AC ADP20070;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human immunodeficiency virus 1 isolate JRCSEF vpr protein.
XX
KW immunogenic mutant HIV gp120; human immunodeficiency virus; HIV; gp120;
KW immunogenic; vaccine; HIV neutralising antibody; anti-HIV;
KW HIV binding agent; immunisation; HIV-1; infection; HIV-1 isolate JRCSEF;
KW VPR.
XX
OS Human immunodeficiency virus 1.
XX
PN WO2004053100-A2.
XX
PD 24-JUN-2004.
XX
PF 11-DEC-2003; 2003WO-US039534.
XX
PR 11-DEC-2002; 2002US-0432869P.
PR 24-APR-2003; 2003US-0465350P.

```

XX (SCRI ) SCRIPPS RES INST.  
 XX Burton DR., Wilson I., Pantophlet R;  
 XX WPI; 2004-480933/45.  
 XX N-PSDB; ADP20074.  
 XX GENBANK; M38429.  
 XX Immunogenic mutant HIV-1 gp120 polypeptide, and antibodies raised against  
 PT the polypeptide, useful preventing or treating human immunodeficiency  
 PT virus (HIV) infection, especially HIV-1 infection.  
 XX Disclosure; Page 138; 149pp; English.  
 XX The present invention describes an immunogenic mutant HIV gp120  
 CC polypeptide that can stimulate a neutralising antibody response against a  
 CC human immunodeficiency virus (HIV). Also described: (1) an immunogenic  
 CC mutant HIV-1 gp120 polypeptide (Ia) that can stimulate a neutralising  
 CC antibody response against a panel of HIV-1 comprising HIV-1 primary  
 CC isolates of at least two different clades, where the mutant gp120 has at  
 CC least one amino acid mutation in at least one epitope of the HIV-1 gp120  
 CC polypeptide specifically bound by a neutralising antibody, which reduces  
 CC binding affinity of the non-neutralising antibody; (2) an immunogenic  
 CC mutant HIV-1 gp120 polypeptide (Ib) having at least one amino acid  
 CC mutation in at least one epitope of the gp120 polypeptide specifically  
 CC bound by a non-neutralising antibody; (3) a vaccine (II) comprising one  
 CC or more (Ia); (4) an antiserum (III) obtained by using (Ib) or (II); (5)  
 CC an isolated HIV neutralising antibody (IV) fraction obtained by using  
 CC (Ib) or (II); (6) a substantially purified HIV neutralising antibody (V)  
 CC obtained by using (Ib) or (II); (7) ameliorating (M1) HIV-1 infection in  
 CC a subject, by administering an HIV neutralising antibody produced in  
 CC response to (Ib); (8) preventing (M2) HIV-1 infection or ameliorating HIV  
 CC -1 infection in a human subject, involves administering HIV-1  
 CC neutralising antibodies to the subject, where the HIV-1 neutralising  
 CC antibodies comprise antibodies stimulated in response to (II); (9) HIV  
 CC neutralising antibodies (VI) produced by using (Ib); (10) isolated HIV  
 CC neutralising antibodies (VII) obtained by using (Ib); and (11) isolated  
 CC HIV-1 neutralising antibodies obtained by harvesting spleen and lymph  
 CC nodes from the mouse immunised by (II). (Ia) and (Ib) have anti-HIV  
 CC activities, and can be used in vaccines and in HIV binding agents. (Ia)  
 CC and (Ib) are useful for inducing antibodies that can neutralise HIV-1  
 CC which involves immunising a subject with a (Ia) or (Ib). The antibodies  
 CC are useful for preventing or ameliorating HIV, especially HIV-1,  
 CC infection in a subject. The present sequence represents an HIV-1 isolate  
 CC JRCSEF vpr protein sequence, which is given in the exemplification of the  
 CC present invention.  
 XX Sequence 96 AA;  
 SQ

Query Match 99.6%; Score 253; DB 8; Length 96;  
 Best Local Similarity 98.0%; Pred. No. 2.1e-29;  
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRRRRNGASRS 49  
 Db 48 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRRRRNGASRS 96  
 RESULT 13  
 ADP81477  
 ID ADP81477 standard; protein; 95 AA.  
 XX  
 AC ADP81477;  
 XX  
 DT 12-AUG-2004 (first entry)  
 DE HIV-1 vpr protein.  
 XX  
 KW vaccine; vpr; HIV-1; HIV infection; ds; gene.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX

PN US6706268-B1.  
 XX  
 PD 16-MAR-2004.  
 XX  
 PF 13-NOV-2000; 2000US-00709316.  
 XX  
 PR 18-OCT-1984; 84PR-00016013.  
 PR 16-NOV-1984; 84GB-00029099.  
 PR 30-AUG-1985; 85US-00771248.  
 PR 22-FEB-1988; 88US-00158652.  
 PR 05-NOV-1992; 92US-00953060.  
 PR 14-FEB-1994; 94US-00195024.  
 PR 31-DEC-1997; 97US-00344449.  
 XX  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CENT NAT RECH SCI.  
 XX  
 PI Alison M, Sonigo P, Stewart C, Danos O, Wain-Hobson S;  
 XX  
 DR WPI; 2004-236717/22.  
 DR N-PSDB; ADP81478.  
 XX  
 PT New purified peptide encoded by the vpr gene of HIV-1, useful for  
 PT preparing a composition for diagnosing or treating HIV infection.  
 XX  
 PS Claim 1; Col 10; 37pp; English.  
 XX  
 CC The invention relates to a new purified peptide encoded by the vpr gene  
 CC of HIV-1 is free of particles of the virus. The peptide is useful for  
 CC preparing a composition for diagnosing or treating HIV infection. The  
 CC present sequence represents the HIV-1 vpr protein.  
 XX  
 SQ Sequence 95 AA;  
 Query Match 98.4%; Score 250; DB 8; Length 95;  
 Best Local Similarity 98.0%; Pred. No. 5.7e-29;  
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRRRRNGASRS 49  
 Db 47 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRRRRNGASRS 95  
 RESULT 14  
 AAR94544  
 ID AAR94544 standard; protein; 96 AA.  
 XX  
 AC AAR94544;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 17-OCT-1996 (first entry)  
 XX  
 DE Native Vpr protein from HIV-1 LAI strain isolate.  
 XX  
 KW Native; Vpr protein; HIV-1 LAI strain isolate; chimeric molecule;  
 KW chimeric; infection; replication; reduction; RNase; protease;  
 KW virion assembly; morphogenesis; steric hindrance inducer; targeted;  
 KW mature virion; structural organisation; gene therapy;  
 KW functional integrity.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN WO9607741-A1.  
 XX  
 PD 14-MAR-1996.  
 XX  
 PF 07-SEP-1995; 95WO-CA000510.  
 XX  
 PR 07-SEP-1994; 94US-00301915.  
 XX  
 PA (UYMO-) UNIV MONTREAL.  
 XX  
 PI Cohen EA, Bergeron D, Checroune F, Yao X, Pignac-Kobinger G;

XX WPI; 1996-171615/17.  
XX Targetting mature HIV virion(s) using HIV Vpr, Vpx or p6 proteins - for  
PT affecting structural organisation or function or for inhibiting  
PT replication.  
XX  
XX Claim 8; Page 43; 68pp; English.  
XX  
XX The present sequence is the native Vpr protein from the HIV-1 LAI strain  
CC isolate, which can be used in the development of a chimaeric mol.  
CC comprising the present sequence and another mol., pref. a HIV infectivity  
CC or replication reducing protein fragment, i.e. a RNase and/or protease, a  
CC virion assembly and/or morphogenesis steric hindrance inducer and/or an  
CC affector of a viral protein interaction responsible for viral infectivity  
CC and/or replication. The chimaeric mol. can be specifically targeted into  
CC the mature HIV-1 virion, to affect its structural organisation and/or  
CC functional integrity, i.e. gene therapy of HIV-1 infection. Vpr protein  
CC fragments can also be used to prevent viral replication by interfering  
CC with the protein interactions responsible for Vpr incorporation into the  
CC mature HIV-1 genome. (Updated on 16-Oct-2003 to standardise OS field)  
XX  
XX Sequence 96 AA;  
SQ

Query Match 98.4%; Score 250; DB 2; Length 96;  
Best Local Similarity 98.0%; Pred. No. 5.8e-29;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLFIHFIRGCRHSRIGVTQRRRNGASRS 49  
Db 48 ETYGDWAGVEAIRILQQLFIHFIRGCRHSRIGVTQRRRNGASRS 96

RESULT 15  
AA53247  
ID AA53247 standard; protein; 96 AA.  
XX  
XX AC AA53247;  
XX  
XX DT 12-SEP-2003 (revised)  
DT 17-JUL-2000 (first entry)  
XX  
XX DE HIV-1 LAI strain Vpr protein SEQ ID NO:1.  
XX  
XX KW HIV-1; HIV-2; virion; Vpr; Vpx; p6; chimeric; infection; anti-HIV;  
KW Gene therapy.  
XX  
XX OS Human immunodeficiency virus 1.  
XX  
XX PN US6043081-A.  
XX  
XX PD 28-MAR-2000.  
XX  
XX PF 07-SEP-1995; 95US-00524694.  
XX  
XX PR 07-SEP-1994; 94US-00301915.  
XX  
XX PA (UYMO-) UNIV MONTREAL.  
XX  
XX FI Yao X, Pignac-Kobinger G, Checroune F, Cohen EA, Bergeron D;  
XX WPI; 2000-270343/23.  
XX  
XX PT Expression vector useful for reducing infectivity of HIV or for targeting  
PT into HIV virions, comprises nucleic acid segment encoding recombinant or  
PT chimeric protein comprising a Vpr/Vpx virion incorporation domain.  
XX  
XX PS Claim 1; Col 7-8; 32pp; English.  
XX  
XX The present invention describes an expression vector (1) comprising a  
CC nucleic acid segment encoding a recombinant protein for interfering with  
CC the incorporation of native Vpr/Vpx into HIV-1 or HIV-2 virion or a  
CC chimeric protein that is incorporated into an HIV-1 or HIV-2 virion,

CC operably linked to a promoter. Also described are: (1) an isolated  
CC eukaryotic or prokaryotic cell transformed with (1); (2) a composition  
CC for reducing infectivity of HIV-1 or HIV-2 in vitro comprising an  
CC effective amount of (1) in association with a pharmaceutically acceptable  
CC carrier; and (3) a composition for targeting into an HIV-1 or HIV-2  
CC virion comprising an effective amount of (1) in association with a  
CC pharmaceutically acceptable carrier. (1) has anti-HIV activity and can be  
CC used in gene therapy. (1) is useful for reducing infectivity of HIV in  
CC vitro and for targeting into an HIV-1 or HIV-2 virion. The present  
CC sequence represents the Vpr protein from an HIV-1 strain, which is used  
CC in the exemplification of the present invention. (Updated on 12-SEP-2003  
CC to standardise OS field)  
XX  
XX Sequence 96 AA;  
SQ

Query Match 98.4%; Score 250; DB 3; Length 96;  
Best Local Similarity 98.0%; Pred. No. 5.8e-29;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLFIHFIRGCRHSRIGVTQRRRNGASRS 49  
Db 48 ETYGDWAGVEAIRILQQLFIHFIRGCRHSRIGVTQRRRNGASRS 96

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Job time : 65.3125 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:42:45 ; Search time 28.5833 Seconds  
(without alignments)  
113.688 Million cell updates/sec

Title: US-09-913-927D-3

Perfect score: 254

Sequence: 1 ETYGDWAGVEAIRILQQL.....RHSRIGVTRQRRNGASRS 49

Scoring table: BLOSUM62

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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254	100.0	96	4	US-09-309-572-19
2	254	100.0	96	4	US-09-718-096-19
3	254	100.0	96	4	US-09-839-329-1
4	250	98.4	96	2	US-08-301-915-1
5	250	98.4	96	3	US-08-524-694A-1
6	250	98.4	96	4	US-09-454-156A-1
7	249	98.0	96	3	US-08-704-856C-15
8	249	98.0	96	4	US-09-242-881-15
9	210.5	82.9	95	4	US-09-319-588C-10
10	197	77.6	100	4	US-09-462-917A-118
11	192	75.6	100	4	US-09-462-917A-115
12	179	70.5	100	4	US-09-462-917A-115
13	172	67.7	93	4	US-09-462-917A-117
14	132	52.0	78	3	US-09-124-900-5
15	131	51.6	72	2	US-08-301-915-4
16	131	51.6	72	3	US-08-524-694A-4
17	131	51.6	72	4	US-09-454-156A-4
18	123	48.4	24	4	US-09-839-329-2
19	119.5	47.0	3077	6	5223423-2
20	117	46.1	100	4	US-09-206-551-49
21	116	45.7	105	2	US-08-301-915-2
22	116	45.7	105	3	US-08-524-694A-2
23	116	45.7	105	4	US-09-454-156A-2
24	105	41.3	105	2	US-08-659-251-9
25	105	41.3	105	3	US-09-256-490-9
26	105	41.3	105	5	PCT-US96-11445-9
27	94	37.0	18	4	US-09-839-329-3

Sequence 58, Appl  
Sequence 58, Appl  
Sequence 58, Appl  
Sequence 38, Appl  
Sequence 10, Appl  
Sequence 106, App  
Sequence 128, Appl  
Sequence 7, Appl  
Sequence 37, Appl  
Sequence 5911, Ap  
Sequence 24912, A  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 29104, A  
Sequence 29150, A  
Sequence 25736, A  
Sequence 30, Appl  
Sequence 30, Appl

28 74 29.1 13 2 US-08-484-905-58  
29 74 29.1 13 3 US-08-481-985B-58  
30 74 29.1 13 3 US-08-370-476-58  
31 74 29.1 13 3 US-08-992-877-38  
32 73 28.7 16 5 PCT-US94-02191-10  
33 72 28.3 15 4 US-09-009-953-106  
34 70 27.6 15 4 US-09-009-953-128  
35 63 24.8 16 5 PCT-US94-02191-7  
36 62 24.4 14 3 US-08-992-877-37  
37 62 24.4 112 4 US-09-621-976-5911  
38 57 22.4 218 4 US-09-252-991A-24912  
39 54.5 21.5 723 4 US-09-849-334-2  
40 54.5 21.5 723 4 US-10-274-878-2  
41 53 20.9 245 4 US-09-252-991A-29404  
42 52.5 20.7 265 4 US-09-252-991A-29150  
43 52.5 20.7 651 4 US-09-252-991A-25736  
44 52 20.5 9 1 US-07-841-662-30  
45 52 20.5 9 1 US-08-209-797-30

#### ALIGNMENTS

##### RESULT 1

US-09-309-572-19  
; Sequence 19, Application US/09309572  
; Patent No. 6440730  
; GENERAL INFORMATION:  
; APPLICANT: Heinrich-Pette-Institut  
; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV  
; FILE REFERENCE: P50489  
; CURRENT APPLICATION NUMBER: US/09/309,572  
; CURRENT FILING DATE: 1999-05-11  
; EARLIER APPLICATION NUMBER: DE 198 56 463  
; EARLIER FILING DATE: 1998-11-26  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: vpr protein  
; US-09-309-572-19

Query Match 100.0%; Score 254; DB 4; Length 96;  
Best Local Similarity 100.0%; Pred. No. 7e-31;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49

Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

##### RESULT 2

US-09-718-096-19  
; Sequence 19, Application US/09718096  
; Patent No. 6585763  
; GENERAL INFORMATION:  
; APPLICANT: Von Laer, Meike-Dorothee  
; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV  
; FILE REFERENCE: 35-195  
; CURRENT APPLICATION NUMBER: US/09/718,096  
; CURRENT FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: DE 19856463.5  
; PRIOR FILING DATE: 1998-11-26  
; PRIOR APPLICATION NUMBER: EP 99250415.9  
; PRIOR FILING DATE: 1999-11-25  
; PRIOR APPLICATION NUMBER: US 09/309,572  
; PRIOR FILING DATE: 1999-05-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19

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; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: vpr protein
US-09-718-096-19

Query Match      100.0%; Score 254; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 7e-31;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 3
US-09-839-329-1
; Sequence 1, Application US/09839329
; Patent No. 6664040
; GENERAL INFORMATION:
; APPLICANT: Michael P. Sherman
; APPLICANT: Warner C. Greene
; APPLICANT: Carlos M.C. de No. 6664040ohna
; APPLICANT: Ulrich Schubert
; APPLICANT: Peter Henklein
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF
; FILE REFERENCE: GSC 30448.91-US-U2
; CURRENT APPLICATION NUMBER: US/09/839,329
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/206,610
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/267,827
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide of regulatory virus proteins R
; OTHER INFORMATION: (vpr) of human immunodeficiency virus type 1
; OTHER INFORMATION: (HIV-1)
US-09-839-329-1

Query Match      100.0%; Score 254; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 7e-31;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 4
US-08-301-915-1
; Sequence 1, Application US/08301915
; Patent No. 5861161
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS
; TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
```

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; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,915
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
US-08-301-915-1

Query Match      98.4%; Score 250; DB 2; Length 96;
Best Local Similarity 98.0%; Pred. No. 2.8e-30;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 5
US-08-524-694A-1
; Sequence 1, Application US/08524694A
; Patent No. 6043081
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED
; TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524,694A
; FILING DATE: September 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
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Qy 1 ETYGDTWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRANGASRS 49
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Db 48 ETYGDTWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRANGASRS 96
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RESULT 7
US-08-704-856C-15
; Sequence 15, Application US/08704856C
; Patent No. 6042832
; GENERAL INFORMATION:
; APPLICANT: Koprowski, Hilary
; APPLICANT: Yusibov, Vidadi
; APPLICANT: Hooper, Douglas, C.
; APPLICANT: Modelska, Anna
; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
; TITLE OF INVENTION: Coat Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allan H. Fried & Associates
; STREET: 1525 Locust Street, 15th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Corel WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,856C
; FILING DATE: 28-Aug-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: N
US-08-704-856C-15

Query Match 98.0%; Score 249; DB 3; Length 96;
Best Local Similarity 98.0%; Pred. No. 4e-30;
Matches 48; Conservative 1; Mismatches 0; Indels 0

Qy 1 ETYGDTWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRANGASRS 49
|||
Db 48 ETYGDTWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRANGASRS 96
|||

RESULT 8
US-09-242-881-15
; Sequence 15, Application US/09242881
; Patent No. 6448070
; GENERAL INFORMATION:
; APPLICANT: Koprowski, Hilary
; APPLICANT: Yusibov, Vidadi
; APPLICANT: Hooper, Douglas, C.
; APPLICANT: Modelska, Anna
; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
; TITLE OF INVENTION: Coat Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allan H. Fried & Associates
; STREET: 1525 Locust Street, 15th Floor
; CITY: Philadelphia

```

```

; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Corel WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/242,881
; FILING DATE: 25-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,856
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHEICAL: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-242-881-15

Query Match          98.0%; Score 249; DB 4; Length 96;
Best Local Similarity 98.0%; Pred. No. 4e-30;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVVAIRILQOLLFIHFRICGRHSRIGVTRQRRAGRS 49
DB 48 ETYGDWTAGVVAIRILQOLLFIHFRICGRHSRIGVTRQRRAGRS 96

RESULT 9
US-09-319-588C-10
; Sequence 10, Application US/09319588C
; Patent No. 6509018
; GENERAL INFORMATION:
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE-INSERM
; APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX DE PARIS
; APPLICANT: INSTITUT PASTEUR
; APPLICANT: MAUCLERE, Philippe
; APPLICANT: LOUSSERT-AJAKA, Ibtissem
; APPLICANT: SIMON, Francois
; APPLICANT: SARAGOSTI, Sentob
; APPLICANT: BARRE-SIMOUSSI, Francoise
; TITLE OF INVENTION: NON-M NON-O HIV STRAINS, FRAGMENTS AND APPLICATIONS.
; FILE REFERENCE: 598U512
; CURRENT APPLICATION NUMBER: US/09/319,588C
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: FR96/15087
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 10
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-319-588C-10

Query Match          82.9%; Score 210.5; DB 4; Length 95;
Best Local Similarity 85.4%; Pred. No. 2.7e-24;
Matches 41; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 2 TYGDTWAGVVAIRILQOLLFIHFRICGRHSRIGVTRQRRAGRS 49

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Query Match 51.6%; Score 131; DB 2; Length 72;  
Best Local Similarity 100.0%; pred. No. 2.2e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILOQLLFHF 25  
Db 48 ETYGDWAGVEAIRILOQLLFHF 72

Search completed: October 18, 2004, 18:49:23  
Job time : 29.5833 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:43:30 ; Search time 88.8125 seconds  
(without alignments)  
178.383 Million cell updates/sec

Title: US-09-913-927D-3  
Perfect score: 254  
Sequence: 1 ETYGDWAGVEAIRILQQL.....RHSRIGVTRQRRAAGSRS 49

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 32318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254	100.0	96	9	US-09-839-329-1
2	254	100.0	96	14	US-10-059-261-272
3	254	100.0	96	14	US-10-190-435-284
4	240	94.5	96	14	US-10-190-435-272
5	239	94.1	96	14	US-10-190-435-285
6	238	93.7	96	14	US-10-190-435-282
7	235	92.5	96	14	US-10-190-435-274
8	235	92.5	96	14	US-10-190-435-278
9	234	92.1	96	14	US-10-190-435-263
10	234	92.1	96	14	US-10-190-435-273
11	234	92.1	96	14	US-10-190-435-276
12	233	91.7	96	14	US-10-190-435-264
13	233	91.7	96	14	US-10-190-435-265
14	233	91.7	96	14	US-10-190-435-266

Sequence 270, App  
Sequence 271, App  
Sequence 256, App  
Sequence 257, App  
Sequence 283, App  
Sequence 4, Appl  
Sequence 1475, App  
Sequence 258, App  
Sequence 259, App  
Sequence 260, App  
Sequence 267, App  
Sequence 2, Appl  
Sequence 268, App  
Sequence 11, Appl  
Sequence 36, Appl  
Sequence 275, App  
Sequence 282, App  
Sequence 277, App  
Sequence 261, App  
Sequence 280, App  
Sequence 254, App  
Sequence 255, App  
Sequence 279, App  
Sequence 10, Appl  
Sequence 281, App  
Sequence 229, App  
Sequence 293, App  
Sequence 51, Appl  
Sequence 1476, App  
Sequence 231, App

ALIGNMENTS

RESULT 1  
US-09-839-329-1  
; Sequence 1, Application US/09839329  
; Publication No. US20020022027A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael P. Sherman  
; APPLICANT: Warner C. Greene  
; APPLICANT: Carlos M.C. de No. 6664040ohna  
; APPLICANT: Ulrich Schubert  
; APPLICANT: Peter Henklein  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF  
; FILE REFERENCE: G&C 30448.91-US-U2  
; CURRENT APPLICATION NUMBER: US/09/839,329  
; CURRENT FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/206,610  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/267,827  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide of regulatory virus proteins R  
; OTHER INFORMATION: (vpr) of human immunodeficiency virus type 1  
; OTHER INFORMATION: (HIV-1)  
US-09-839-329-1  
Query Match 100.0%; Score 254; DB 9; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.5e-28;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLFIHFHRCRHSRIGVTRQRRAAGSRS 49  
|||||

Db 48 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 96

## RESULT 2

; Sequence 272, Application US/10059261  
; Publication No. US20030077826A1  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS  
; APPLICANT: BRIAND, JEAN-PAUL  
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET  
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC  
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX  
; TITLE OF INVENTION: (PTPC)  
; FILE REFERENCE: 03495.0216  
; CURRENT APPLICATION NUMBER: US/10/059,261  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/265,594  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 325  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 272  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-10-059-261-272

Query Match 100.0%; Score 254; DB 14; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.5e-28;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 49  
|||||  
Db 48 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 96

## RESULT 3

US-10-190-435-284  
; Sequence 284, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: PP18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 284  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Vpr HXB2  
US-10-190-435-284

Query Match 100.0%; Score 254; DB 14; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.5e-28;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 49  
|||||  
Db 48 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 96

## RESULT 4

US-10-190-435-272

; Sequence 272, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: PP18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 272  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV005-81  
US-10-190-435-272

Query Match 94.5%; Score 240; DB 14; Length 96;  
Best Local Similarity 89.8%; Pred. No. 1.6e-26;  
Matches 44; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 49  
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Db 48 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 96

## RESULT 5

US-10-190-435-285  
; Sequence 285, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: PP18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 285  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus  
US-10-190-435-285

Query Match 94.1%; Score 239; DB 14; Length 96;  
Best Local Similarity 91.8%; Pred. No. 2.2e-26;  
Matches 45; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 49  
|||||  
Db 48 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 96

## RESULT 6

US-10-190-435-262  
; Sequence 262, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.

; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: PP18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; SOFTWARE: PatentIn Ver. 2.0  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 262  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV004-45  
US-10-190-435-262

Query Match 93.7%; Score 238; DB 14; Length 96;  
Best Local Similarity 89.8%; Pred. No. 3e-26;  
Matches 44; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTGVAEAIIRILQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 49  
Db 48 ETYGDWTGVAEAIIRVLQQLLFTHFRIGCRHSRIGILQORRRNGASRS 96

RESULT 7  
US-10-190-435-274  
; Sequence 274, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: PP18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 274  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV006-9  
US-10-190-435-274

Query Match 92.5%; Score 235; DB 14; Length 96;  
Best Local Similarity 87.8%; Pred. No. 8.2e-26;  
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTGVAEAIIRILQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 49  
Db 48 ETYGDWTGVAEAIIRVLQQLLFTHFRIGCRHSRIGILQORRRNGASRS 96

RESULT 8  
US-10-190-435-278  
; Sequence 278, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

; FILE REFERENCE: PP18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 278  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Vpr 301905-Ind  
US-10-190-435-278

Query Match 92.5%; Score 235; DB 14; Length 96;  
Best Local Similarity 89.8%; Pred. No. 8.2e-26;  
Matches 44; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ETYGDWTGVAEAIIRILQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 49  
Db 48 ETYGDWTGVTETIRILQQLLFTHFRIGCRHSRIGILQORRRNGASRS 96

RESULT 9  
US-10-190-435-263  
; Sequence 263, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: PP18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 263  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV001-2  
US-10-190-435-263

Query Match 92.1%; Score 234; DB 14; Length 96;  
Best Local Similarity 87.8%; Pred. No. 1.1e-25;  
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTGVAEAIIRILQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 49  
Db 48 ETYGDWTGVAEAIIRVLQQLLFTHFRIGCRHSRIGILQORRRNGASRS 96

RESULT 10  
US-10-190-435-273  
; Sequence 273, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: PP18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 273
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV012-4
US-10-190-435-273

Query Match          92.1%; Score 234; DB 14; Length 96;
Best Local Similarity 91.7%; Pred. No. 1.1e-25;
Matches 44; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYGDTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRRNGASRS 49
Db 49 TYGDTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRRNGASRS 96

RESULT 11
US-10-190-435-276
; Sequence 276, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 276
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr 92BR025
US-10-190-435-276

Query Match          92.1%; Score 234; DB 14; Length 96;
Best Local Similarity 91.7%; Pred. No. 1.1e-25;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRRNGASRS 49
Db 48 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRRNGASRS 96

RESULT 12
US-10-190-435-264
; Sequence 264, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 264
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV002-84
US-10-190-435-264
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV018-7
US-10-190-435-264

Query Match          91.7%; Score 233; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 1.6e-25;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRRNGASRS 49
Db 48 DTYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRRNGASRS 96

RESULT 13
US-10-190-435-265
; Sequence 265, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 265
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV018-8
US-10-190-435-265

Query Match          91.7%; Score 233; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 1.6e-25;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRRNGASRS 49
Db 48 DTYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRRNGASRS 96

RESULT 14
US-10-190-435-266
; Sequence 266, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 266
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV002-84
US-10-190-435-266

Query Match          91.7%; Score 233; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 1.6e-25;
```



Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQQLLFIHFRIGCRHSRIGVTQRARRNGASRS 49  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 48 DTYGDTWGWGVEAIRILQQLLFIHFRIGCQHSRIGVTQRARRNGASRS 96

RESULT 15  
US-10-190-435-270  
; Sequence 270, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: PP18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 270  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV003-12  
US-10-190-435-270

Query Match 91.7%; Score 233; DB 14; Length 96;  
Best Local Similarity 87.8%; Pred. No. 1.6e-25;  
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQQLLFIHFRIGCRHSRIGVTQRARRNGASRS 49  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 48 DTYGDTWGWGVEAIRILQQLLFIHFRIGCQHSRIGVTQRARRNGASRS 96

Search completed: October 18, 2004, 18:52:23  
Job time : 89.8125 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:38:31 ; Search time 17.3542 Seconds  
(without alignments)  
271.671 Million cell updates/sec

Title: US-09-913-927D-3  
Perfect score: 254  
Sequence: 1 ETYGDWTWAGVEAIRILQQL.....RHGRIGVTRQRRRNGASRS 49

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249	98.0	96	2 T09444	vpr protein - huma
2	244	96.1	96	2 S54380	vpr protein - huma
3	235	92.5	96	2 T01670	vpr protein - huma
4	233.5	91.9	95	2 T09383	vpr protein - huma
5	228.5	90.0	97	1 D44001	vpr protein - huma
6	205	80.7	96	1 ASLJSC	vpr protein - simi
7	120	47.2	89	2 S07991	vpr protein - simi
8	120	47.2	101	2 T11563	vpr protein - simi
9	120	47.2	105	2 S53095	vpr protein - huma
10	118	46.5	101	2 S08439	vpr protein - huma
11	117	46.1	122	1 ASLJRS	vpr protein - simi
12	116	45.7	105	1 ASLJRS	vpr protein - huma
13	115	45.3	101	1 ASLJRS	vpr protein - simi
14	113	44.5	104	1 ASLJCY	vpr protein - huma
15	111	43.7	97	2 S03087	gene R protein - h
16	110.5	43.5	104	1 ASLJSY	vpr protein - huma
17	110	43.3	105	1 ASLJGR	vpr protein - huma
18	108	42.5	105	2 S12156	vpr protein - huma
19	67.5	26.6	119	1 ASLJX4	vpu protein - simi
20	56.5	22.2	314	2 C97332	ABC-type transport
21	55.5	21.9	178	2 T42536	hypothetical prote
22	54.5	21.5	328	2 H81996	probable integral
23	54.5	21.5	328	2 H81225	hypothetical prote
24	54.5	21.5	454	2 A13467	glycine betaine/1-
25	53.5	21.1	275	2 B55224	hypothetical prote
26	53.5	21.1	311	2 H95877	hypothetical prote
27	53	20.9	532	2 G84427	hypothetical prote
28	52.5	20.7	341	2 F69171	conserved hypothet
29	51.5	20.3	282	2 C69553	conserved hypothet

30	51.5	20.3	292	2 F86431	hypothetical prote
31	51.5	20.3	328	2 A72379	hypothetical prote
32	51.5	20.3	399	2 T40877	hypothetical prote
33	51	20.1	449	2 J01277	triacylglycerol li
34	50.5	19.9	226	2 F72108	amino acid ABC tra
35	50.5	19.9	226	2 G86514	ABC amino acid tra
36	50.5	19.9	659	2 T20753	hypothetical prote
37	50	19.7	96	2 AE1328	hypothetical prote
38	50	19.7	147	2 B87606	hypothetical prote
39	50	19.7	180	2 A42283	hypothetical prote
40	50	19.7	342	2 AD3391	alcohol dehydrogen
41	50	19.7	354	2 B87288	GTP-binding protei
42	50	19.7	408	2 AF2118	hypothetical prote
43	50	19.7	753	2 A96747	probable RNA-bindi
44	50	19.7	910	2 E89918	2-oxoglutarate deh
45	49.5	19.5	72	2 D61055	E5b protein - huma

ALIGNMENTS

RESULT 1

T09444  
vpr protein - human immunodeficiency virus type 1 (strain JRPL)  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T09444  
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,  
submitted to the EMBL Data Library, July 1996  
A;Reference number: Z16673  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Accession: T09444  
A;Molecule type: DNA  
A;Residues: 1-96 <PAN>  
A;Cross-references: UNIPROT:Q75757; EMBL:U63632; NID:g1465777; PID:g1465784  
C;Genetics:  
A;Gene: vpr  
C;Superfamily: AIDS vpr protein

Query Match 98.0%; Score 249; DB 2; Length 96;  
Best Local Similarity 95.9%; Pred. No. 7.6e-28;  
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRRNGASRS 49  
|||||  
Db 48 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRRNGASRS 96  
|||||

RESULT 2

S54380  
vpr protein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S54380  
R;Theodore, T.; Buckler-White, A.J.  
submitted to the EMBL Data Library, July 1989  
A;Reference number: S54377  
A;Accession: S54380  
A;Status: preliminary  
A;Molecule type: genomic RNA  
A;Residues: 1-96 <THE>  
A;Cross-references: UNIPROT:P12519; EMBL:M22639; NID:g329377; PIDN:AAA45368.1; PID:g329377  
C;Superfamily: AIDS vpr protein

Query Match 96.1%; Score 244; DB 2; Length 96;  
Best Local Similarity 91.8%; Pred. No. 3.8e-27;  
Matches 45; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRRNGASRS 49  
|||||  
Db 48 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRRNGSSRS 96  
|||||

## RESULT 3

T01670  
vpr protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: T01670  
R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.  
Cell 46, 63-74, 1986  
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates  
A:Reference number: Z14389; MUID:86245056; PMID:2424612  
A:Accession: T01670  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-96 <ALI>  
A:Cross-references: UNIPROT:P05955; EMBL:K03456; NID:G60228; PIDN:CAA28014.1; PID:G60232  
C:Superfamily: AIDS vpr protein

Query Match 92.5%; Score 235; DB 2; Length 96;  
Best Local Similarity 89.8%; Pred. No. 7.2e-26;  
Matches 44; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 49  
|||||  
DB 48 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 96  
|||||

## RESULT 4

T09383  
vpr protein - human immunodeficiency virus type 1 (isolate cntrl 1)  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate cntrl 1  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T09383  
R:Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bir  
J. Virol. 69, 4228-4236, 1995  
A:Title: Defective accessory genes in a human immunodeficiency virus type 1-infected lon  
A:Reference number: Z16654; MUID:95287475; PMID:7769682  
A:Accession: T09383  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-95 <MTC>  
A:Cross-references: UNIPROT:Q71925; EMBL:U24451; NID:G829440; PIDN:AAA79575.1; PID:G8294

Query Match 91.9%; Score 233.5; DB 2; Length 95;  
Best Local Similarity 93.9%; Pred. No. 1.2e-25;  
Matches 46; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 49  
|||||  
DB 48 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 95  
|||||

## RESULT 5

D44001  
vpr protein - human immunodeficiency virus type 1 (strain YU-2)  
N:Alternate names: orf-R protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: D44001  
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.  
J. Virol. 66, 6587-6600, 1992

A:Title: Complete nucleotide sequence, genome organization, and biological properties of  
A:Reference number: A44001; MUID:93021387; PMID:1404505  
A:Accession: D44001  
A:Molecule type: DNA  
A:Residues: 1-97 <LIY>  
A:Cross-references: UNIPROT:P35967; GB:M93258  
C:Genetics:

A:Gene: vpr  
C:Superfamily: AIDS vpr protein  
C:Keywords: AIDS; immunodeficiency

Query Match 90.0%; Score 228.5; DB 1; Length 97;  
Best Local Similarity 90.0%; Pred. No. 6e-25;  
Matches 45; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 49  
|||||  
DB 48 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 97  
|||||

## RESULT 6

ASLJSC  
vpr protein - simian immunodeficiency virus SIVcpz  
N:Alternate names: orf-R protein  
C:Species: simian immunodeficiency virus SIVcpz  
A:Note: host Pan troglodytes (chimpanzee)  
C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: S09986  
R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.  
Nature 345, 356-359, 1990  
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.  
A:Reference number: S09983; MUID:90259077; PMID:2188136  
A:Accession: S09986  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-96 <HUE>  
A:Cross-references: UNIPROT:P17287; EMBL:X52154; NID:G58866; PIDN:CAA36403.1; PID:G58870  
C:Genetics:

A:Gene: vpr  
C:Superfamily: AIDS vpr protein  
C:Keywords: AIDS; immunodeficiency

Query Match 80.7%; Score 205; DB 1; Length 96;  
Best Local Similarity 75.5%; Pred. No. 1.3e-21;  
Matches 37; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 49  
:|||||  
DB 48 DTYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 96  
:|||||

## RESULT 7

S07991  
vpr protein - simian immunodeficiency virus SIVsm (isolate F236)  
C:Species: simian immunodeficiency virus SIVsm  
A:Note: host Cercopithecus torquatus atys (sooty mangabey)  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S07991  
R:Hirsch, V.M.; Olmsted, R.A.; Murphy-Corb, M.; Purcell, R.H.; Johnson, P.R.  
Nature 339, 389-392, 1989  
A:Title: An African primate lentivirus (SIV(sm)) closely related to HIV-2.  
A:Reference number: S04237; MUID:89262053; PMID:2786147  
A:Accession: S07991  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: genomic RNA  
A:Residues: 1-89 <HIR>  
A:Cross-references: UNIPROT:P12521; EMBL:X14307; NID:G61741; PIDN:CAA32486.1; PID:G61745  
A:Note: this sequence was submitted to the EMBL Data Library, February 1989  
C:Genetics:

A:Gene: vpr  
C:Superfamily: AIDS vpr protein

Query Match 47.2%; Score 120; DB 2; Length 89;  
Best Local Similarity 60.5%; Pred. No. 1.2e-09;  
Matches 23; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTR 38  
:|||||  
DB 49 DRHGTLSGAGELIRILQRLFIHFRSCAHSRIGQSR 86  
:|||||

```
RESULT 8
T11563
vpr protein - simian immunodeficiency virus SIVsm (strain E543)
C;Species: simian immunodeficiency virus SIVsm
A;Variety: strain E543
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11563
R;Hirsch, V.M.; Adger-Johnson, D.; Cambell, B.; Goldstein, S.; Brown, C.; Elkins, W.R.;
J. Virol. 71, 1608-1620, 1997
A;Title: A molecularly cloned, pathogenic, neutralization-resistant simian immunodeficiency
A;Reference number: 217285; MUID:97151152; PMID:8995688
A;Accession: T11563
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-101 <HIR>
A;Cross-references: UNIPROT:P89157; EMBL:U72748; NID:gl695908; PIDN:AAC56562.1; PID:gl695
C;Genetics:
A;Gene: vpr
C;Superfamily: AIDS vpr protein
C;Keywords: AIDS; immunodeficiency

Query Match 47.2%; Score 120; DB 2; Length 101;
Best Local Similarity 60.5%; Pred. No. 1.4e-09;
Matches 23; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVEAIRILQQLLFHFRIGCRHSRIGVTR 38
:|||||:|||||:|||||:|||||:|||||:
DB 49 DRHGDTEGAGELIRILQALFHFHFRSGCAHSRIGQSR 86
:|||||:|||||:|||||:|||||:|||||:

RESULT 9
S53095
vpr protein - human immunodeficiency virus type 2
C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53095
R;Becker, M.; Zorr, B.; Becker, A.; Habermehl, K.O.
submitted to the EMBL Data Library, March 1995
A;Description: Molecular and phylogenetic characterisation of a Guinea-Bissau-derived hu
A;Reference number: S53091
A;Accession: S53095
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <BEC>
A;Cross-references: UNIPROT:Q76624; EMBL:Z48731; NID:G732718; PIDN:CAAB88624.1; PID:G7327
C;Superfamily: AIDS vpr protein

Query Match 47.2%; Score 120; DB 2; Length 105;
Best Local Similarity 63.9%; Pred. No. 1.4e-09;
Matches 23; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 3 YGDTWAGVEAIRILQQLLFHFRIGCRHSRIGVTR 38
:|||||:|||||:|||||:|||||:|||||:
DB 55 HGDTLEGARELIRLQALFTHFRAGCGHSRIGQTR 90
:|||||:|||||:|||||:|||||:|||||:

RESULT 10
S08439
vpr protein - human immunodeficiency virus type 2 D205
C;Species: human immunodeficiency virus type 2 D205, HIV-2 D205
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S08439
R;Dietrich, U.; Adamaki, M.; Kreutz, R.; Seipp, A.; Kuehnelt, H.; Ruebeamen-Waigmann, H.
Nature 342, 948-950, 1989
A;Title: A highly divergent HIV-2-related isolate.
A;Reference number: S08434; MUID:90081881; PMID:2594088
A;Accession: S08439
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <DIE>
A;Cross-references: UNIPROT:P15837; EMBL:X16109
A;Note: this sequence was submitted to the EMBL Data Library, Aug-1989
```

```
C;Genetics:
A;Gene: vpr
C;Superfamily: AIDS vpr protein

Query Match 46.5%; Score 118; DB 2; Length 101;
Best Local Similarity 63.6%; Pred. No. 2.6e-09;
Matches 21; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 YGDTWAGVEAIRILQQLLFHFRIGCRHSRIG 35
:|||||:|||||:|||||:|||||:|||||:
DB 55 HGDTLAGAGELIKLQALFHFHFRAGCQHSRIG 87
:|||||:|||||:|||||:|||||:|||||:

RESULT 11
ASLJR3
vpr protein - simian immunodeficiency virus SIVagm (type 3, isolate STLIV-3agm)
N;Alternate names: orf-R protein
C;Species: simian immunodeficiency virus SIVagm
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: E26737
R;Hirsch, V.; Riedel, N.; Mullins, J.I.
Cell 49, 307-319, 1987
A;Title: The genome organization of STLIV-3 is similar to that of the AIDS virus except for
A;Reference number: A26737; MUID:87187627; PMID:3646094
A;Accession: E26737
A;Molecule type: DNA
A;Residues: 1-122 <HIR>
A;Cross-references: UNIPROT:P11265; GB:M19499; NID:G334657
C;Genetics:
A;Gene: vpr
C;Superfamily: AIDS vpr protein
C;Keywords: AIDS; immunodeficiency

Query Match 46.1%; Score 117; DB 1; Length 122;
Best Local Similarity 57.5%; Pred. No. 4.4e-09;
Matches 23; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 3 YGDTWAGVEAIRILQQLLFHFRIGCRHSRIGVTRORRA 42
:|||||:|||||:|||||:|||||:|||||:
DB 51 HGDTLEGAGELIRLQALFHFHFRGCGNHSRIGQTWGRKS 90
:|||||:|||||:|||||:|||||:|||||:

RESULT 12
ASLJR2
vpr protein - human immunodeficiency virus type 2 (isolate ROD)
N;Alternate names: orf-R protein
C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: H26262
R;Guyader, M.; Emerman, M.; Sonigo, P.; Clavel, F.; Montagnier, L.; Allizon, M.
Nature 326, 662-669, 1987
A;Title: Genome organization and transactivation of the human immuno-deficiency virus ty
A;Reference number: A26262; MUID:87173056; PMID:3031510
A;Accession: H26262
A;Molecule type: DNA
A;Residues: 1-105 <GUY>
A;Cross-references: UNIPROT:P06938; GB:M15390; NID:gl332361; PIDN:AAB00767.1; PID:G32574
C;Genetics:
A;Gene: vpr
C;Superfamily: AIDS vpr protein
C;Keywords: AIDS; immunodeficiency

Query Match 45.7%; Score 116; DB 1; Length 105;
Best Local Similarity 58.3%; Pred. No. 5.2e-09;
Matches 21; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 3 YGDTWAGVEAIRILQQLLFHFRIGCRHSRIGVTR 38
:|||||:|||||:|||||:|||||:|||||:
DB 55 HGDTLEGARELIKVLQALFTHFRAGCGHSRIGQTR 90
:|||||:|||||:|||||:|||||:|||||:

RESULT 13
ASLJR3
```

```

vpr protein - simian immunodeficiency virus (macaque isolate)
N:Alternate names: orf-R protein
C:Species: simian immunodeficiency virus, SIV
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C:Accession: E28887
R:Chakrabarti, L.; Guyader, M.; Allizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P.
A:Title: Sequence of simian immunodeficiency virus from macaque and its relationship to
A:Reference number: A28887; MUID:87287230; PMID:3649576
A:Accession: E28887
A:Molecule type: DNA
A:Residues: 1-101 <CHA>
A:Cross-references: GB:Y00277; GB:M16403; NID:g61730; PIDN:CAA68383.1; PID:g61735
C:Genetics:
A:Gene: vpr
C:Superfamily: AIDS vpr protein
C:Keywords: AIDS; immunodeficiency

Query Match 45.3%; Score 115; DB 1; Length 101;
Best Local Similarity 66.7%; Pred. No. 7e-09; Mismatches 3; Indels 0; Gaps 0;
Matches 22; Conservative 3;

QY 3 YGDTWAGVEAIRILQQLLFHFRIGCRHSRIG 35
:|||||:|||||:|||||:|||||:|||||
DB 51 HGDTEGAGELIRILQALFTHFRSGCHSRIG 83

RESULT 14
ASLVCY
vpr protein - human immunodeficiency virus type 2 (isolate CAM2/Guinea-Bissau)
N:Alternate names: orf-R protein
C:Species: human immunodeficiency virus type 2, HIV-2
A:Note: host Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: E38475; JQ0977
R:Tristem, M.; Hill, F.; Karpas, A.
J. Gen. Virol. 72, 721-724, 1991
A:Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus type
A:Reference number: A38475; MUID:91170959; PMID:2005437
A:Accession: E38475
A:Molecule type: DNA
A:Residues: 1-104 <TRI>
A:Cross-references: UNIPROT:P24111; GB:D00835; NID:g3153166; PIDN:BAA00713.1; PID:g22147
C:Genetics:
A:Gene: vpr
C:Superfamily: AIDS vpr protein
C:Keywords: AIDS; immunodeficiency

Query Match 44.5%; Score 113; DB 1; Length 104;
Best Local Similarity 58.3%; Pred. No. 1.4e-08;
Matches 21; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 3 YGDTWAGVEAIRILQQLLFHFRIGCRHSRIGVTR 38
:|||||:|||||:|||||:|||||:|||||
DB 55 HGDTERARELIRVLRALFTHFRAGCNHSRIGQTR 90

RESULT 15
S03067
Gene R protein - human T-cell lymphotropic virus type 4
C:Species: human T-cell lymphotropic virus type 4, HTLV-4
C>Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S03067
R:Hahn, B.H.; Kong, L.I.; Lee, S.W.; Kumar, P.; Taylor, M.E.; Arya, S.K.; Shaw, G.M.
Nature 300, 184-186, 1987
A:Title: Relation of HTLV-4 to simian and human immunodeficiency-associated viruses.
A:Reference number: S03065
A:Accession: S03067
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-97 <HAH>
A:Cross-references: UNIPROT:Q85605; EMBL:X06391; NID:g61580; PIDN:CAA29689.1; PID:g61582
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1987

```

C:Superfamily: AIDS vpr protein

Query Match 43.7%; Score 111; DB 2; Length 97;  
Best Local Similarity 63.6%; Pred. No. 2.5e-08;  
Matches 21; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 3 YGDTWAGVEAIRILQQLLFHFRIGCRHSRIG 35  
:|||||:|||||:|||||:|||||:|||||  
DB 51 HGDTEGAGELIRILQALFTHFRSGCHSRIG 83

Search completed: October 18, 2004, 18:48:21  
Job time : 18.3542 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:34:40 ; Search time 61.25 Seconds  
(without alignments)  
460.300 Million cell updates/sec

Title: US-09-913-927D-3  
Perfect score: 254  
Sequence: 1 ETYGDWTWAGVEAIRILQQL.....RHSRIGVTRRRRANGASRS 49

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	254	100.0	96	1 VPR_HV1NS	P12520 human immun
2	253	99.6	96	1 VPR_HV1JR	P20883 human immun
3	253	99.6	96	2 O6SZU3	O6SZU3 human immun
4	253	99.6	96	2 O9IBN7	O9IBN7 human immun
5	253	99.6	96	2 AAR24628	AAR24628 human imm
6	252	99.2	96	2 O71267	O71267 human immun
7	252	99.2	96	2 O90307	O90307 human immun
8	251	98.8	96	2 O6Q440	O6Q440 human immun
9	251	98.8	96	2 AAS86190	AAS86190 human imm
10	250	98.4	96	1 VPR_HV1BR	P05928 human immun
11	250	98.4	96	2 O9IQB8	O9IQB8 human immun
12	249	98.0	96	1 VPR_HV1RH	P05954 human immun
13	249	98.0	96	2 O36203	O36203 human immun
14	249	98.0	96	2 O6JN73	O6JN73 human immun
15	249	98.0	96	2 O6SZU2	O6SZU2 human immun
16	249	98.0	96	2 O6SZU5	O6SZU5 human immun
17	249	98.0	96	2 O71939	O71939 human immun
18	249	98.0	96	2 O72014	O72014 human immun
19	249	98.0	96	2 O75757	O75757 human immun
20	249	98.0	96	2 O79234	O79234 human immun
21	249	98.0	96	2 O79245	O79245 human immun
22	249	98.0	96	2 O7SU29	O7SU29 human immun
23	249	98.0	96	2 O7SV42	O7SV42 human immun
24	249	98.0	96	2 O6H1N6	O6H1N6 human immun
25	249	98.0	96	2 O7ZJ96	O7ZJ96 human immun
26	249	98.0	96	2 O89636	O89636 human immun
27	249	98.0	96	2 O9IQA5	O9IQA5 human immun
28	249	98.0	96	2 O9IQA6	O9IQA6 human immun
29	249	98.0	96	2 O9IQA8	O9IQA8 human immun
30	249	98.0	96	2 O9IQA9	O9IQA9 human immun
31	249	98.0	96	2 O9IQB0	O9IQB0 human immun

32	249	98.0	96	2	O9IQB1	Q9IQB1 human immun
33	249	98.0	96	2	O9IQC6	Q9IQC6 human immun
34	249	98.0	96	2	Q900A1	Q900A1 human immun
35	249	98.0	96	2	Q902S8	Q902S8 human immun
36	249	98.0	96	2	AAR24626	AAR24626 human imm
37	249	98.0	96	2	AAR24629	AAR24629 human imm
38	249	98.0	96	2	AAQ98596	AAQ98596 human imm
39	248	97.6	96	2	O71277	O71277 human immun
40	248	97.6	96	2	O6SZT9	O6SZT9 human immun
41	248	97.6	96	2	O79247	O79247 human immun
42	248	97.6	96	2	O7ZJF0	O7ZJF0 human immun
43	248	97.6	96	2	O6E889	O6E889 human immun
44	248	97.6	96	2	AAR24632	AAR24632 human imm
45	247	97.2	96	1	VPR_HV1MN	P05950 human immun

ALIGNMENTS

RESULT 1  
VPR\_HV1NS STANDARD; PRT; 96 AA.  
AC P12520;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE VPR protein (R ORF protein).  
GN Name=VPR;  
OS Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
ON NCBI\_TaxID=11698;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCov J.;  
RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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EMBL; M19921; AAA44990.1; -;  
DR PDB; 1BDE; NMR; @=49-83.  
DR PDB; 1DSJ; NMR; @=49-76.  
DR PDB; 1DSK; NMR; @=59-86.  
DR PDB; 1KZS; NMR; A=33-52.  
DR PDB; 1KZT; NMR; A=33-52.  
DR PDB; 1KZV; NMR; A=33-52.  
DR HIV; M19921; VPR\$NL43  
DR InterPro; IPR000012; Retrov\_vpr/X.  
DR Pfam; PF00522; VPR; 1.  
DR PRINTS; PR00444; HIVPRVPX.  
KW 3D-structure; AIDS.  
FT HELIX 52 78  
SQ SEQUENCE 96 AA; 11379 MW; 58BC53573479D150 CRC64;

Query Match 100.0%; Score 254; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 7.4e-27;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ETYGDWTWAGVEAIRILQQLFTHFRIGCHSHSRIQVTRRRRANGASRS 49  
|||||  
Db 48 ETYGDWTWAGVEAIRILQQLFIHFRIGCHSHSRIQVTRRRRANGASRS 96  
|||||

RESULT 2  
VPR\_HV1JR STANDARD; PRT; 96 AA.  
ID\_VPR\_HV1JR  
AC P20883;  
DT 01-FEB-1991 (Rel. 17, Created)

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DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE VPR protein (R ORF protein).
GN Name=VPR;
OS Human immunodeficiency virus type 1 (JRCSP isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; M38429; AAB03747.1; -
DR HSP; P12520; 1BDE.
DR HIV; M38429; VPRJRCSP.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRPX.
KW AIDS.
SQ SEQUENCE 96 AA; 11419 MW; 06954E578BED2925 CRC64;
Query Match 99.6%; Score 253; DB 1; Length 96;
Best Local Similarity 98.0%; Pred. No. 1e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETYGDWTAGVVAIRIQLQLLFHFRICGRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWTAGVVAIRIQLQLLFHFRICGRHSRIGVTRQRRARNGASRS 96
RESULT 3
Q6SZU3 PRELIMINARY; PRT; 96 AA.
AC Q6SZU3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Vpr protein.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Rodas B., Toro C., Paxinos E., Poveda E., Martinez-Padial M.,
RA Benito J.M., Jimenez V., Wrin T., Basani S., Soriano V.;
RT "Differences in disease progression in a cohort of long-term non-
RT progressors after more than 16 years of HIV-1 infection."
RL AIDS 18:1109-1116(2004).
DR EMBL; AY444321; AAR24628.1; -
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRPX.
KW AIDS.
SQ SEQUENCE 96 AA; 11353 MW; 9576F43AFEDB1244 CRC64;
Query Match 99.6%; Score 253; DB 2; Length 96;
Best Local Similarity 98.0%; Pred. No. 1e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETYGDWTAGVVAIRIQLQLLFHFRICGRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWTAGVVAIRIQLQLLFHFRICGRHSRIGVTRQRRARNGASRS 96
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RESULT 4
Q9IBN7 PRELIMINARY; PRT; 96 AA.
ID Q9IBN7;
AC Q9IBN7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VPR protein.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Vella C., Smith M.H., Farrar G.H., Jones D.H., Daniels R.S.;
RT "A molecular and serologic study of the envelope gene of the British
RT isolate: HIV-1 GB8."
RL Vaccine 13:735-741(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farrar G.H., Roff M.A., Amin T., Ball J., Parrett A.M.,
RA Battacharya U., Booth J., Wansbrough-Jones M.H., Greenaway P.J.;
RT "Characterisation of a series of human immunodeficiency virus isolates
RT derived sequentially from a single patient."
RL J. Med. Virol. 34:104-113(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Novelli P., Vella C., Oxford J.S., Daniels R.S.;
RT "Biological characterization of an infectious molecular clone of HIV
RT Type 1GB8."
RL AIDS Res. Hum. Retroviruses 16:1175-1178(2000).
DR EMBL; AJ271445; CAB92789.1; -
DR HSP; P12520; 1BDE.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
KW AIDS.
FT CHAIN 1 20 vif.
FT CHAIN 1 96 vpr.
FT CHAIN 91 96 tat.
SQ SEQUENCE 96 AA; 11293 MW; C00C5A439E0DD92E CRC64;
Query Match 99.6%; Score 253; DB 2; Length 96;
Best Local Similarity 98.0%; Pred. No. 1e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETYGDWTAGVVAIRIQLQLLFHFRICGRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWTAGVVAIRIQLQLLFHFRICGRHSRIGVTRQRRARNGASRS 96
RESULT 5
AAR24628 PRELIMINARY; PRT; 96 AA.
ID AAR24628;
AC AAR24628;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Vpr protein.
GN VPR.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9;
```



```
RA Rodas B., Toro C., Paxinos E., Poveda E., Martinez-Padial M.,
RT Jimenez V., Wrin T., Bassani S., Soriano V.;
RT "Differences in disease progression in a cohort of long-term non-
RT progressors after more than 15 years of HIV-1 infection.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY444321; AAR24628.1; -.
SQ SEQUENCE 96 AA; 11353 MW; 9576F43AFEDB1244 CRC64;

Query Match          99.6%; Score 253; DB 2; Length 96;
Best Local Similarity 98.0%; Pred. No. 1e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 6
ID O71267 PRELIMINARY; PRT; 96 AA.
AC O71267;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Oelrichs R.B., McPhee D.A., Deacon N.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042103; AAD03219.1; -.
DR HSP; P12520; IDSJ.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
SQ SEQUENCE 96 AA; 11349 MW; AE455A5E25808256 CRC64;

Query Match          99.2%; Score 252; DB 2; Length 96;
Best Local Similarity 95.9%; Pred. No. 1.4e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 7
ID Q903U7 PRELIMINARY; PRT; 96 AA.
AC Q903U7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes D.I., Ashton L., Solomon A., Carr A., Cooper D., Kaldor J.,
RA Deacon N.;
RT "Characterization of three nef-defective HIV-1 strains associated with
RT long term nonprogression.";
RL J. Virol. 0:0-0(2000).
DR EMBL; AY006000; AAG32143.1; -.
DR HSP; P12520; IDSJ.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.

RA Rodas B., Toro C., Paxinos E., Poveda E., Martinez-Padial M.,
RT Jimenez V., Wrin T., Bassani S., Soriano V.;
RT "Differences in disease progression in a cohort of long-term non-
RT progressors after more than 15 years of HIV-1 infection.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY444321; AAR24628.1; -.
SQ SEQUENCE 96 AA; 11346 MW; C1BD60F1048E5036 CRC64;

Query Match          99.2%; Score 252; DB 2; Length 96;
Best Local Similarity 95.9%; Pred. No. 1.4e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 8
ID Q6Q440 PRELIMINARY; PRT; 96 AA.
AC Q6Q440;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Vpr protein.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Sanchez G.I., Carrion G., Eyzaguirre L., Arias S., Negrete M.,
RA Montano S., Perez J., Russell K.L., Sateren W., Birx D.L., Carr J.K.,
RA Sanchez J.L.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY561244; AAS86190.1; -.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
SQ SEQUENCE 96 AA; 11242 MW; F7893B5D57E14C2C CRC64;

Query Match          98.8%; Score 251; DB 2; Length 96;
Best Local Similarity 95.9%; Pred. No. 1.9e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 9
ID AAS86190 PRELIMINARY; PRT; 96 AA.
AC AAS86190;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Vpr protein.
GN VPR.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCM031;
RA Sanchez G.I., Carrion G., Eyzaguirre L., Arias S., Negrete M.,
RA Montano S., Perez J., Russell K.L., Sateren W., Birx D.L., Carr J.K.,
RA Sanchez J.L.;
RT "Molecular and epidemiological characterization of HIV-1 infected
RT individuals from Medellin, Columbia.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY561244; AAS86190.1; -.
SQ SEQUENCE 96 AA; 11242 MW; F7893B5D57E14C2C CRC64;

Query Match          98.8%; Score 251; DB 2; Length 96;
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Best Local Similarity 95.9%; Pred. No. 1.9e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVGAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
|||||
Db 48 ETYGDWTAGVGAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 10
ID VPR_HV1BR STANDARD; PRT; 96 AA.
AC P05928;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE VPR protein (R ORF protein).
GN Names=VPR;
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
RT "Nucleotide sequence of the AIDS virus, LAV.";
RL Cell 40:9-17(1985).
RN [2]
RP SEQUENCE FROM N.A. (CLONE PNL4-3).
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; K02013; AAB59749.1; -.
DR HSSP; P12520; 1BDE.
DR HIV; K02013; VPR$BRU.
DR HIV; M19921; VPR$NL43.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT CONFLICT 15 15 H -> Y (in Ref. 2).
FT CONFLICT 28 28 N -> S (in Ref. 2).
FT CONFLICT 41 41 G -> N (in Ref. 2).
FT CONFLICT 85 85 Q -> R (in Ref. 2).
SQ SEQUENCE 96 AA; 11295 MW; 42892A4186583D3E CRC64;

Query Match 98.4%; Score 250; DB 1; Length 96;
Best Local Similarity 98.0%; Pred. No. 2.6e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVGAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
|||||
Db 48 ETYGDWTAGVGAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 11
Q9IOB8 PRELIMINARY; PRT; 96 AA.
ID Q9IOB8;
AC Q9IOB8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein.
GN Names=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
```

```
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20338596; PubMed=10881687;
RA Yamada T., Iwamoto A.;
RT "Comparison of proviral accessory genes between long-term
RT nonprogressors and progressors of human immunodeficiency virus type 1
RT infection.";
RL Arch. Virol. 145:1021-1027(2000).
DR EMBL; AB034527; BAA93974.1; -.
DR HSSP; P12520; 1BDE.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
SQ SEQUENCE 96 AA; 11365 MW; 9EAAF998E0B6DD80 CRC64;

Query Match 98.4%; Score 250; DB 2; Length 96;
Best Local Similarity 95.9%; Pred. No. 2.6e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVGAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
|||||
Db 48 ETYGDWTAGVGAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 12
VPR_HV1RH STANDARD; PRT; 96 AA.
ID VPR_HV1RH STANDARD; PRT; 96 AA.
AC P05954;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE VPR protein (R ORF protein).
GN Name=VPR;
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-staal F.;
RT "Identification and characterization of conserved and variable regions
RT in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";
RL Cell 45:637-648(1986).
CC -----
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CC -----
CC EMBL; M17451; AAA45055.1; -.
DR PDB; 1F10; NMR; A=12-33.
DR HIV; M17451; VPR$RF.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW 3D-structure; AIDS.
SQ SEQUENCE 96 AA; 11338 MW; 85BC4E4D5CF17741 CRC64;

Query Match 98.0%; Score 249; DB 1; Length 96;
Best Local Similarity 95.9%; Pred. No. 3.6e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVGAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
|||||
Db 48 ETYGDWTAGVGAIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96
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**RESULT 13**

036203	PRELIMINARY;	PRT;	96 AA.
ID	O36203		
AC	O36203;		
DT	01-JAN-1998	(TREMBLrel. 05, Created)	
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)	
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)	
DE	Vpr protein.		
GN	Name=Vpr;		
OS	Human immunodeficiency virus 1.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxId=11676;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Song J., Wang B., Ge Y.C., Dwyer D., Dowton D., Cunningham A.,		
RA	Saksena N.;		
RL	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF000315; AAB70154.1;		
DR	HSSP; P12520; 1DSJ.		
DR	InterPro; IPR000012; RetroV_Vpr/X.		
DR	Fam; PF00522; VPR; 1.		
DR	PRINTS; PR00444; HIVVPRVPX.		
KW	AIDS.		
SQ	SEQUENCE	96 AA; 11349 MW; 06954E5151109B4C	CRC64:

Query Match 98.0%; Score 249; DB 2; Length 96;  
Best Local Similarity 95.9%; Pred. No. 3.6e-26;  
Matches 47; Conservative 2; Mismatches 0; Indels 0

Qy 1 ETYGD TWAGVEAIIRILQOLLFIHFRCGRHSRIGVTRQRRRNGASRS 49

Db 48 ETYGD TWAGVEAIIRILQOLLFIHFRCGRHSRIGVTRQRRRNGASRS 96

## RESULT 14

Q6JN73	PRELIMINARY;	PRT;	96 AA.
ID	Q6JN73		
AC	Q6JN73;		
DT	05-JUL-2004	(TEMBLrel. 27, Created)	
DT	05-JUL-2004	(TEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TEMBLrel. 27, Last annotation update)	
DE	Vpr protein.		
GN	Names=vpr;		
OS	Human immunodeficiency virus 1.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11676;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PubMed=15186520;		
RA	Tovanabutra S., Beyrer C., Sakthachornphop S., Razak M.H., Ramos G.L.,		
RA	Vongchak T., Rungvuthanakit K., Sakhieo P., Tejjafong K., Kim B.,		
RA	De Souza M., Robb M.L., Birx D.L., Jittiwutikarn J., Suriyanon V.,		
RA	Calentano D.D., McCutchan F.E.;		
RT	"The Changing Molecular Epidemiology of HIV Type 1 among Northern Thai		
RT	Drug Users, 1999 to 2002."		
RL	AIDS Res. Hum. Retroviruses 20:465-475(2004).		
RL	EMBL; AY358073; AAQ98596.1; -		
DR	InterPro; IPR000012; Retrov_Vpr/X.		
DR	Pfam; PF00522; VPR; 1.		
DR	PRINTS; PR00444; HIVPRVFX.		
KW	AIDS.		
SD	SEQUENCE 96 AA; 11205 MW; 9B009C38EB30B7EE CRC64;		

Query Match 98.0%; Score 249; DB 2; Length 96;  
Best Local Similarity 95.9%; Pred. NO. 3.6e-26;  
Matches 47; Conservative 2; Mismatches 0; Indels

Qy 1 ETYGDTWAGVEAIIRILQQLLFHFRTICCRHSRIGVTRQRRRNGASRS 49  
 |||||  
 Db 48 ETYGDTWAGVEAIIRILQQLLFHFRTICCRHSRIGVTRQRRRNGASRS 96  
 |||||

## RESULT 15

## 0657112

ID	Q6S2U2	PRELIMINARY;	PRT;	96 AA.
AC	Q6S2U2;			
DC	05-JUL-2004 (TReMBLrel. 27, Created)			
DT	05-JUL-2004 (TReMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)			
DE	Vpr protein.			
DN	Name=vpr;			
OS	Human immunodeficiency virus 1.			
GC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OC	NCBI_TaxId=11676;			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RX	PubMed=15166526;			
RA	Rodes B., Toro C., Paxinos E., Poveda E., Martinez-Padial M., Benito J. M., Jimenez V., Wrin T., Bassani S., Soriano V.;			
RT	"Differences in disease progression in a cohort of long-term non-progressors after more than 16 years of HIV-1 infection.";			
RL	AIDS 18:1109-1116(2004).			
DR	EMBL; AV444322; AAR24629.1;			
DR	InterPro; IPR000012; RetroV_Vpr/X.			
DR	Pfam; PF00522; VPR; 1.			
DR	PRINTS; PR00444; HIVVPRVPX.			
DR	AIDS.			
SK	SEQUENCE	96 AA; 11338 MW; 85BC4E49PB617244 CRC64;		
QW				

Query Match	98.0%	Score 249;	DB 2;	Length 96;
Best Local Similarity	95.9%	Pred. No. 3.6e-26;		
Matches 47;	Conservative	2;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy	1	ETYGDTWAGVEAIIRILQQLLFIFHRICGRHSRIGVTRRRRNGASRS	49
	11		
	48	ETYGDTWAGVEAIIRILQQLLFIFHRICGRHSRIGVTRRRRNGASRS <td>96</td>	96
D <sub>b</sub>			

Search completed: October 18, 2004, 18:47:47  
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